

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SPARKS, Andrew B.
HOFFMAN, Noah
KAY, Brian K.
FOWLKES, Dana M.
McCONNELL, Stephen J.
- (ii) TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
- (iii) NUMBER OF SEQUENCES: 227
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/630,915
 - (B) FILING DATE: 03-APR-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Misrock, S. Leslie
 - (B) REGISTRATION NUMBER: 18,872
 - (C) REFERENCE/DOCKET NUMBER: 1101-174
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (D) OTHER INFORMATION: May or may not have carboxy-terminal
 amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

Ser Gly Ser Gly Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr  
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Gly Ser Gly Ser Arg Leu Thr Pro Gln Ser Lys Pro Pro Leu Pro.  
1 5 10 15

Pro Lys Pro Ser Trp Val Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GTGAATGCTG CAGACAGTGA CGGATGGACA CCACTGCATT GTGCTGCCTC TTGCAACAGT 60
GTCCACCTCT GCAAGCAGCT GGTGGAAAGT GGAGCCGCTA TCTTTGCCTC CACCATCAGT 120
GACATTGAGA CTGCTGCAGA CAAGTGTGAA GAGATGGAAG AGGGATACAT CCAGTGTTC 180
CAGTTTCTGT ATGGGGTACA AGAGAAGCTG GGAGTGATGA ACAAAGGCAC CGTGTATGCT 240
TTGTGGGACT ACGAGGCCCA GAACAGCGAT GAGCTGTCCT TCCATGAAGG GGATGCCATC 300
ACCATCCTGA GGCGCAAAGA TGAAAACGAG ACCGAGTGGT GGTGGGCTCG TCTTGGGGAC 360
CGGGAGGGCT ACGTGCCCAA AAACCTTGCTG GGGTTGTATC CACGGATCAA ACCCCGGCAG 420
CGAACACTTG CCTGAACCCC CTGGAGTACC ACAGTCTCGT TTGCTCCCAG GAGCTACTGG 480
AGGAGATCCC ACTGCCCTGG GAAAAC TGAA GCTAGGATGG TCTCCTGGTG CTCACTTTAG 540
CAGACAGTGT CCACAATGTG AATCCCACTT CCCAGGTGAG GCCCTCTCCA GGCTGCAGGA 600
GCTGG 605

```

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Val Asn Ala Ala Asp Ser Asp Gly Trp Thr Pro Leu His Cys Ala Ala
1 5 10 15
Ser Cys Asn Ser Val His Leu Cys Lys Gln Leu Val Glu Ser Gly Ala
20 25 30
Ala Ile Phe Ala Ser Thr Ile Ser Asp Ile Glu Thr Ala Ala Asp Lys
35 40 45
Cys Glu Glu Met Glu Glu Gly Tyr Ile Gln Cys Ser Gln Phe Leu Tyr
50 55 60
Gly Val Gln Glu Lys Leu Gly Val Met Asn Lys Gly Thr Val Tyr Ala
65 70 75 80
Leu Trp Asp Tyr Glu Ala Gln Asn Ser Asp Glu Leu Ser Phe His Glu
85 90 95

```

Gly Asp Ala Ile Thr Ile Leu Arg Arg Lys Asp Glu Asn Glu Thr Glu  
                   100                                  105                                  110  
 Trp Trp Trp Ala Arg Leu Gly Asp Arg Glu Gly Tyr Val Pro Lys Asn  
                   115                                  120                                  125  
 Leu Leu Gly Leu Tyr Pro Arg Ile Lys Pro Arg Gln Arg Thr Leu Ala  
                   130                                  135                                  140

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GAATTCAAGC TCGGGTTGCG CGCGGTCCGG AGCGGCCGCG GCCAGCGCAG GCTTGGCGCC  | 60   |
| CAGTTGTCGT GTGCGTGTGG GGCTCCCGCG GCTGAGCCTG GTCGCTCCGT GTAGCGCCAT  | 120  |
| GTCCAAGCCA CCTCCCAAC CGGTCAAACC AGGGCAAGTT AAAGTCTTCA GAGCTCTATA   | 180  |
| TACATTTGAA CCCAGAACTC CAGATGAATT ATACTTTGAA GAAGGAGACA TTATCTACAT  | 240  |
| CACTGACATG AGTGATACCA GCTGGTGGAA AGGGACATGC AAGGGCAGAA CAGGACTGAT  | 300  |
| CCCGAGCAAC TATGTGGCTG AGCAGGCAGA ATCCATTGAC AATCCATTGC ATGAAGCTGC  | 360  |
| AAAAAGAGGC AACCTGAGCT GGTTGAGGGA GTGCTTGGAC AACCGGGTGG GTGTGAACGG  | 420  |
| CCTGGACAAA GCTGGAAGCA CAGCCCTGTA CTGGGCCTGC CACGGTGGCC ATAAAGACAT  | 480  |
| AGTGAGAGTT CTGTTTACTC AGCCGAATGT GGAGCTGAAC CAGCAGAATA AGCTGGGAGA  | 540  |
| CACAGCTCTG CACGCGGNTG CCTGGAAGGG TTATGCAGAC ATTGTCAGT TGCTACTGGC   | 600  |
| AAAAGGTGCG AGGACAGACT TGAGAAACAA TGAGAAGAAG CTGGCCTTGG ACATGGCCAC  | 660  |
| CAACGCTGCC TGTGCATCGC TCCTGAAGAA GAAGCAGCAG GGAACAGATG GGGCTCGAAC  | 720  |
| GTTAAGCAAC GCCGAGGACT ACCTCGATGA CGAAGACTCA GACTGATTCC CCCCAGGGGCC | 780  |
| GCTTTGATTG TTGCCTAAAC TTCTTTTGCT TTTGCCATTC CGGAGCCTGG GTTGTGTTGCC | 840  |
| AGAAGAGTAT TGATAACTGT TGCTTTTAAA GTCTGTATGA GCGCGACACT GCTGCACTGT  | 900  |
| GATCTGTGAG GAGTCGTTGT GAGGGTGGCT CATTCTCACC CACGCCTTGN CAATAAGTGA  | 960  |
| AGAGATACTT TGTTGTATAA AATACATATA TGCTCACCAG GGTAAAATAA ACGAAAAAAA  | 1020 |
| NTTATTTCTA TTTATCAAGC TAAAAAATAA AAGCTTGGGC CCTNTTCTAT AGTGTCACCT  | 1080 |
| AAATACTAGC TTGANCCGGN TGCTAACAAA GCCCGAAAGG AAGCTGAGTT GCTGCTGCCA  | 1140 |
| CCGNTGAGCA ATAAC TAGCA TANCCCCCTG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT | 1200 |
| NGNTGAAAGG AGGANCTATT TCCGATAAC CTGGNGTAAT AGGGAAGAGG CCCGNACCGA   | 1260 |
| TCGCCCTTCC CAACAGA                                                 | 1277 |



(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Cys Ala Arg Ser Gly Ala Ala Ala Ser Ala Gly Leu Ala  
1 5 10 15  
Pro Ser Cys Arg Val Arg Val Gly Leu Pro Arg Leu Ser Leu Val Ala  
20 25 30  
Pro Cys Ser Ala Met Ser Lys Pro Pro Pro Lys Pro Val Lys Pro Gly  
35 40 45  
Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro  
50 55 60  
Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met  
65 70 75 80  
Ser Asp Thr Ser Trp Trp Lys Gly Thr Cys Lys Gly Arg Thr Gly Leu  
85 90 95  
Ile Pro Ser Asn Tyr Val Ala Glu Gln Ala Glu Ser Ile Asp Asn Pro  
100 105 110  
Leu His Glu Ala Ala Lys Arg Gly Asn Leu Ser Trp Leu Arg Glu Cys  
115 120 125  
Leu Asp Asn Arg Val Gly Val Asn Gly Leu Asp Lys Ala Gly Ser Thr  
130 135 140  
Ala Leu Tyr Trp Ala Cys His Gly Gly His Lys Asp Ile Val Glu Val  
145 150 155 160  
Leu Phe Thr Gln Pro Asn Val Glu Leu Asn Gln Gln Asn Lys Leu Gly  
165 170 175  
Asp Thr Ala Leu His Ala Ala Ala Trp Lys Gly Tyr Ala Asp Ile Val  
180 185 190  
Gln Leu Leu Leu Ala Lys Gly Ala Arg Thr Asp Leu Arg Asn Asn Glu  
195 200 205  
Lys Lys Leu Ala Leu Asp Met Ala Thr Asn Ala Ala Cys Ala Ser Leu  
210 215 220  
Leu Lys Lys Lys Gln Gln Gly Thr Asp Gly Ala Arg Thr Leu Ser Asn  
225 230 235 240  
Ala Glu Asp Tyr Leu Asp Asp Glu Asp Ser Asp  
245 250

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTCACGNCG GTGGAGTGGT ACCGGATCGA ATTCAAGCCG CATCACTGGC ACTGGACGCC  | 60  |
| AGGGCATCTT CCCTGCCAGC TACGTGCAGA TAAACCGAGA GCGCCGGCTC AGGCTTTGTG  | 120 |
| ATGATGGTCC CCAGCTCCCT GCATCACCTA ACCCGACAAC CACTGCTCAC CTAAGCAGCC  | 180 |
| ACTCCCACCC CTCCTCAATA CCTGTGGACC CCACTGACTG GGGAGGTCGA ACCTCCCCCTC | 240 |
| GACGCTCCGC CTTTCCCTTC CCCATCACCC TCCAGGAGCC CAGATCCCAA ACCCAGAGTC  | 300 |
| TCAATACCCC TGGACCAACC CTGTCCCATC CTCGAGCCAC CAGCCGTCCC ATAAACCTGG  | 360 |
| GACCCTCCTC CCCAAACACA GAGATACACT GGACTCCGTA CCGGGCCATG TACCAGTACA  | 420 |
| GGCCCCAGAA TGAGGACGAG CTGGAACCTC GAGAGGGGGA CCGTGTGGAT GTCATGCAGC  | 480 |
| AATGTGACGA TGGCTGGTTT GTGGGTGTCT CCCGGCGAAC TCAGAAATTT GGGACATTCC  | 540 |
| CTGGAATTA TGTAGCCCCA GTGTGAGTGG TCTCCATGGC AGTTTGGAGC CAACGAGGAT   | 600 |
| CGGGAGGGGA GCAGTAGCAC TATGGGAGGG AGAGAGGCCT TCCATAGCCT CCTCCCCAGG  | 660 |
| ACCTGTGCTC CCAGCTTCTG CAGAGACCCC AGCAACTTTC CCTCCAAGCC TCCTTGAAGT  | 720 |
| CCGATTCCCA CCGCAAGT CACAGGCATT CCTTTGACAG CCCCCTTCAC CGCCCCCTCAA   | 780 |
| ATACAGACAT CTGCTTTCAT GTGGNAAAA AAAAAAATT AAAAGGTGGC CCTAT         | 835 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Thr | Gly | Thr | Gly | Arg | Gln | Gly | Ile | Phe | Pro | Ala | Ser | Tyr | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ile | Asn | Arg | Glu | Pro | Arg | Leu | Arg | Leu | Cys | Asp | Asp | Gly | Pro | Gln |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Pro | Ala | Ser | Pro | Asn | Pro | Thr | Thr | Thr | Ala | His | Leu | Ser | Ser | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | His | Pro | Ser | Ser | Ile | Pro | Val | Asp | Pro | Thr | Asp | Trp | Gly | Gly | Arg |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Ser | Pro | Arg | Arg | Ser | Ala | Phe | Pro | Phe | Pro | Ile | Thr | Leu | Gln | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Arg | Ser | Gln | Thr | Gln | Ser | Leu | Asn | Thr | Pro | Gly | Pro | Thr | Leu | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Pro | Arg | Ala | Thr | Ser | Arg | Pro | Ile | Asn | Leu | Gly | Pro | Ser | Ser | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Asn Thr Glu Ile His Trp Thr Pro Tyr Arg Ala Met Tyr Gln Tyr Arg  
 115 120 125  
 Pro Gln Asn Glu Asp Glu Leu Glu Leu Arg Glu Gly Asp Arg Val Asp  
 130 135 140  
 Val Met Gln Gln Cys Asp Asp Gly Trp Phe Val Gly Val Ser Arg Arg  
 145 150 155 160  
 Thr Gln Lys Phe Gly Thr Phe Pro Gly Asn Tyr Val Ala Pro Val  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTNNNNYYMM SKYSKKGKKK KGKWSGRTC GATTCAAGCC GACCAGCGGC GGCCCGGCGA  | 60   |
| CCCCAGCCGC CTCTCCGCAT CTGCATCTGC ATCTGCCGGC CGCGCAGCCT CCCGCATCCC | 120  |
| ATCATGTCGG TGGCAGGGCT GAAGAAGCAG TTCCACAAAG CCACTCAGAA AGTGAGTGAG | 180  |
| AAGGTGGGAG GAGCGGAAGG CACCAAGCTC GATGATGACT TCAAAGAGAT GGAGAGGAAA | 240  |
| GTGGATGTCA CCAGCAGGGC TGTGATGGAG ATAATGACAA AAACGATTGA ATACCTCCAA | 300  |
| CCCAATCCAG CTTCCAGGGC TAAGCTCAGT ATGATCAACA CCATGTCGAA AATCCGCGGC | 360  |
| CAAGAGAAGG GGCCAGGCTA CCCTCAGGCG GAAGCACTGC TGGCAGAGGC CATGCTCAAG | 420  |
| TTCGGCAGGG AGCTGGGTGA TGATTGCAAC TTTGGTCCTG CTCTCGGTGA GGTGGGAGAA | 480  |
| GCCATGAGGG AGCTCTCGGA GGTCAAGGAC TCATTGGACA TGGAAGTGAA GCAGAATTTC | 540  |
| ATCGACCCCC TTCAGAATCT TCATGACAAG GATCTGAGGG AGATTCAGCA TCATCTGAAA | 600  |
| AAGCTGGAAG GCCGACGCTT AGACTTTGGT TATAAGAAGA AGCGACAAGG CAAGATTCCA | 660  |
| GATGAAGAAC TCCGCCAAGC TCTGGAGAAA TTCGATGAGT CTAAAGAAAT CGCCGAGTCG | 720  |
| AGCATGTTCA ACCTCTTGGA GATGGATATA GAACAGGTGA GCCAGCTCTC CGCACTTGTT | 780  |
| CAGGCTCAGC TGGAGTACCA CAAGCAGGCA GTGCAGATCC TGCAGCAGGT CACTGTCAGA | 840  |
| CTGGAAGAAA GAATAAGACA AGCTTCATCT CAGCCAAGAA GGGAATATCA GCCCAAACCA | 900  |
| CGGATGAGCC TAGAGTTTGC CACTGGAGAC AGTACTCAGC CCAACGGGGG TCTCTCCCAC | 960  |
| ACAGGCACAC CCAAACCTCC AGGTGTCCAA ATGGATCAGC CCTGCTGCCG AGCTCTGTAT | 1020 |
| GACTTGGAAC CTGAAAATGA AGGGGAATTG GCTTTTAAAG AGGGCGATAT CATCACACTC | 1080 |
| ACTAATCAGA TTGACGAGAA CTGGTATGAG GGGATGCTTC ATGGCCAGTC TGGCTTTTTC | 1140 |
| CCCATCAACT ATGTAGAAAT TCTGGTTGCT CTGCCCCATT AGGATCCTGT GCTGGCTGGC | 1200 |
| TCACCTCCTT CTGACCCAGA TAGTTAAGTT TAACCACTGC TTTGGTAATG CTGCTTCCAA | 1260 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TACATCACGA ATGCAGGCCG CAGTGGATGA GTCACCAAGC CCACACGTGC CCTGGGTTGA  | 1320 |
| CCCGTGTGCT CCTCCAGGAG ACGCGGTGAT AGATGGTATC TTCCAAGGCC AGTGGGCCCTG | 1380 |
| GTACATGCTT TAAAACACCA TCTGAGACTA GCCAGGAGTC CCAGAACTGG CTTCACAGTT  | 1440 |
| CTCAGGAGGC TGTGGTTCCT GGTAACATGC CTGTGAACCA CATGGCAGAA AAACTCTCCT  | 1500 |
| CACTGAAGAT ATTGTCTCTC ACCCAGGGGC CATCTCAAGG TCTCCAGTTC TCCATTTACA  | 1560 |
| GAGGAGAAAG TCCTTTTTGT TGCACTTTCC CTTCTTAAAT ATGTGAGTCA CAGAATTGTT  | 1620 |
| GGCAAAAACA TCCCCTCACC AGCAAGATGT CTGCTGGTTT AAGCAACTTG GTCTCTTGAT  | 1680 |
| GCCATTAGCA AAAGTATTAA TTGTCCAAAG CACCTTTGTT CACTAATATC TATCTATCTA  | 1740 |
| TCTATCTATC TATCTATCTA TCTATCTATC TATCTATCAT CTATCTACCT ACCTATCTAC  | 1800 |
| CTATCATCTA TCTATCTATC ATCTATTATC TATCTATCTA TCTATCTATC NNTCNATCTA  | 1860 |
| TCTATCTATC CATCTATCTA TCCATCATCT ATCTACCTAC CTATCTACTA TCCATCTATC  | 1920 |
| TATCTATCCA TCATCTATCT ACCTACCTAT CTACTATCCA TCCATTTATC TATCTATCTA  | 1980 |
| TCTATCTATC TATCTATCTA TCTCCCTCAT ACTTCTGAGA CATGGCCAGT TTTCTTCCCT  | 2040 |
| CCCTGCTGTT AAGCACTTGG NAGATGAGGG GGGGGGTCCC ATTTNATTTT TGAGTGAGAT  | 2100 |
| GGTGAGCAGG GTGTATGTTG GCTGTNNTNN GGGGGTGGCC CTA                    | 2143 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ser | Val | Ala | Gly | Leu | Lys | Lys | Gln | Phe | His | Lys | Ala | Thr | Gln | Lys | 1   | 5   | 10  | 15 |
| Val | Ser | Glu | Lys | Val | Gly | Gly | Ala | Glu | Gly | Thr | Lys | Leu | Asp | Asp | Asp | 20  | 25  | 30  |    |
| Phe | Lys | Glu | Met | Glu | Arg | Lys | Val | Asp | Val | Thr | Ser | Arg | Ala | Val | Met | 35  | 40  | 45  |    |
| Glu | Ile | Met | Thr | Lys | Thr | Ile | Glu | Tyr | Leu | Gln | Pro | Asn | Pro | Ala | Ser | 50  | 55  | 60  |    |
| Arg | Ala | Lys | Leu | Ser | Met | Ile | Asn | Thr | Met | Ser | Lys | Ile | Arg | Gly | Gln | 65  | 70  | 75  | 80 |
| Glu | Lys | Gly | Pro | Gly | Tyr | Pro | Gln | Ala | Glu | Ala | Leu | Leu | Ala | Glu | Ala | 85  | 90  | 95  |    |
| Met | Leu | Lys | Phe | Gly | Arg | Glu | Leu | Gly | Asp | Asp | Cys | Asn | Phe | Gly | Pro | 100 | 105 | 110 |    |
| Ala | Leu | Gly | Glu | Val | Gly | Glu | Ala | Met | Arg | Glu | Leu | Ser | Glu | Val | Lys | 115 | 120 | 125 |    |

Asp Ser Leu Asp Met Glu Val Lys Gln Asn Phe Ile Asp Pro Leu Gln  
 130 135 140  
 Asn Leu His Asp Lys Asp Leu Arg Glu Ile Gln His His Leu Lys Lys  
 145 150 155 160  
 Leu Glu Gly Arg Arg Leu Asp Phe Gly Tyr Lys Lys Lys Arg Gln Gly  
 165 170 175  
 Lys Ile Pro Asp Glu Glu Leu Arg Gln Ala Leu Glu Lys Phe Asp Glu  
 180 185 190  
 Ser Lys Glu Ile Ala Glu Ser Ser Met Phe Asn Leu Leu Glu Met Asp  
 195 200 205  
 Ile Glu Gln Val Ser Gln Leu Ser Ala Leu Val Gln Ala Gln Leu Glu  
 210 215 220  
 Tyr His Lys Gln Ala Val Gln Ile Leu Gln Gln Val Thr Val Arg Leu  
 225 230 235 240  
 Glu Glu Arg Ile Arg Gln Ala Ser Ser Gln Pro Arg Arg Glu Tyr Gln  
 245 250 255  
 Pro Lys Pro Arg Met Ser Leu Glu Phe Ala Thr Gly Asp Ser Thr Gln  
 260 265 270  
 Pro Asn Gly Gly Leu Ser His Thr Gly Thr Pro Lys Pro Pro Gly Val  
 275 280 285  
 Gln Met Asp Gln Pro Cys Cys Arg Ala Leu Tyr Asp Leu Glu Pro Glu  
 290 295 300  
 Asn Glu Gly Glu Leu Ala Phe Lys Glu Gly Asp Ile Ile Thr Leu Thr  
 305 310 315 320  
 Asn Gln Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser  
 325 330 335  
 Gly Phe Phe Pro Ile Asn Tyr Val Glu Ile Leu Val Ala Leu Pro His  
 340 345 350

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1867 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CGGGCGCGGC GGGAGCCTGG TGGACCCTGC TTTGGCGGTA ATCATTGATC ATCGCAGATG | 60  |
| CCCTCATATC CACTTTGGAT TCCTTGGATT CGGACAGACT CTGAACTGCT TTTCCCAGCA | 120 |
| AAAGAGAAAG ATGTGGAAAG CCTCTGCAGG CCATGCTGTG TCCATCACGC AGGATGATGG | 180 |
| AGGAGCTGAT GACTGGGAGA CTGATCCTGA TTTTGTGAAT GATGTGAGTG AAAAGGAGCA | 240 |
| GAGATGGGGT GCTAAACCG TGCAGGGATC GGGGCACCAG GAACACATCA ACATTCACAA  | 300 |
| GCTTCGAGAG AATGTCTTCC AAGAACACCA GACGCTCAAG GAGAAGGAGC TGGAAACGGG | 360 |

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| ACCCAAGGCT | TCCCACGGCT | ATGGCGGGAA  | GTTTCGGTGTG | GAGCAGGATA | GGATGGACAG  | 420  |
| ATCAGCCGTG | GGCCATGAGT | ACCACTCGAA  | GCTTTCCAAG  | CACTGCTCAC | AAGTGGACTC  | 480  |
| GGTCCGGGGC | TTCGGAGGCA | AGTTCGGTGT  | CCAGATGGAC  | AGGGTGGATC | AGTCTGCTGT  | 540  |
| AGGCTTTGAA | TACCAGGGGA | AGACTGAGAA  | GCATGCCTCC  | CAGAAAGACT | ACTCTAGTGG  | 600  |
| CTTCGGTGGC | AAATACGGTG | TGCAAGCTGA  | CCGTGTAGAC  | AAGAGTGCCG | TGGGCTTTGA  | 660  |
| CTACCAGGGC | AAGACGGAGA | AGCATGAGTC  | TCAGAAAGAT  | TACTCCAAAG | GTTTTGGTGG  | 720  |
| CAAATATGGG | ATTGACAAGG | ACAAGGTGGA  | TAAAAGTCCT  | GTGGGCTTTG | AGTATCAAGG  | 780  |
| CAAGACAGAG | AAGCACGAAT | CCCAGAAAGA  | CTATGTAAAA  | GGCTTTGGAG | GAAAGTTTGG  | 840  |
| TGTGCAGACA | GACAGACAGG | ACAAGTGTGC  | CCTTGGCTGG  | GACCATCAGG | AGAAGCTGCA  | 900  |
| GCTGCATGAA | TCCCAAAAAG | ACTATAAGAC  | TGGTTTCGGA  | GGCAAATTTG | GTGTTTCAGTC | 960  |
| CGAGAGGCAG | GACTCCTCCG | CTGTGGGGTT  | TGATTACAAG  | GAGAGATTGG | CCAAGCACGA  | 1020 |
| GCCCCAGCAA | GACTATGCCA | AAGGATTCGG  | CGGGAAGTAT  | GGGGTGCAGA | AGGATCGGAT  | 1080 |
| GGACAAGAAT | GCATCCACCT | TTGAAGAAGT  | GGTCCAGGTG  | CCATCTGCCT | ATCAGAAGAC  | 1140 |
| TGTCCCCATT | GAGGCCGTAA | CCAGCAAAAC  | CAGTAATATC  | CGTGCTAACT | TTGAAAACCT  | 1200 |
| GGCAAAGGAG | AGAGAGCAGG | AGGACAGGCG  | GAAGGCAGAA  | GCCGAGAGAG | CTCAGCGGAT  | 1260 |
| GGCCAAAGAA | AGACAGGAGC | AGGAGGAGGC  | GCGCAGGAAG  | CTGGAAGAGC | AAGCCAGAGC  | 1320 |
| CAAGAAGCAG | ACGCCCCCTG | CATCCCCCTAG | TCCTCAACCA  | ATTGAAGACA | GACCACCCTC  | 1380 |
| CAGCCCCATC | TATGAGGATG | CAGCTCCGTT  | CAAGGCCGAG  | CCGAGCTACC | GAGGTAGCGA  | 1440 |
| ACCTGAGCCT | GAGTACAGCA | TCGAGGCCGC  | AGGCATTCTT  | GAGGCTGGCA | GCCAGCAAGG  | 1500 |
| CCTGACCTAT | ACATCAGAGC | CCGTGTACGA  | GACTACAGAG  | GCTCCTGGCC | ACTATCAAGC  | 1560 |
| AGAGGATGAC | ACCTACGATG | GGTATGAGAG  | TGACCTGGGC  | ATCACAGCCA | TCGCCCTGTA  | 1620 |
| TGACTACCAG | GCTGCTGGCG | ATGATGAGAT  | CTCCTTTGAC  | CCTGATGACA | TCATACCAA   | 1680 |
| CATAGAAATG | ATTGACGATG | GCTGGTGGCG  | TGGGGTGTGC  | AAGGGCAGAT | ACGGGCTCTT  | 1740 |
| CCCAGCCAAG | TATGTGGAGC | TGCGGCAGTA  | GGGCTGCCAC  | CCAGAGCCTA | CCGGCACCAG  | 1800 |
| CACAGGGTTC | AACTACAGA  | GCATCTGCGT  | GTGTTTGAGT  | TGGTTTCTGC | TTCCGTTTCT  | 1860 |
| GTTTTTG    |            |             |             |            |             | 1867 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Lys | Ala | Ser | Ala | Gly | His | Ala | Val | Ser | Ile | Thr | Gln | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly Gly Ala Asp Asp Trp Glu Thr Asp Pro Asp Phe Val Asn Asp Val  
 20 25 30  
 Ser Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Val Gln Gly Ser Gly  
 35 40 45  
 His Gln Glu His Ile Asn Ile His Lys Leu Arg Glu Asn Val Phe Gln  
 50 55 60  
 Glu His Gln Thr Leu Lys Glu Lys Glu Leu Glu Thr Gly Pro Lys Ala  
 65 70 75 80  
 Ser His Gly Tyr Gly Gly Lys Phe Gly Val Glu Gln Asp Arg Met Asp  
 85 90 95  
 Arg Ser Ala Val Gly His Glu Tyr Gln Ser Lys Leu Ser Lys His Cys  
 100 105 110  
 Ser Gln Val Asp Ser Val Arg Gly Phe Gly Gly Lys Phe Gly Val Gln  
 115 120 125  
 Met Asp Arg Val Asp Gln Ser Ala Val Gly Phe Glu Tyr Gln Gly Lys  
 130 135 140  
 Thr Glu Lys His Ala Ser Gln Lys Asp Tyr Ser Ser Gly Phe Gly Gly  
 145 150 155 160  
 Lys Tyr Gly Val Gln Ala Asp Arg Val Asp Lys Ser Ala Val Gly Phe  
 165 170 175  
 Asp Tyr Gln Gly Lys Thr Glu Lys His Glu Ser Gln Lys Asp Tyr Ser  
 180 185 190  
 Lys Gly Phe Gly Gly Lys Tyr Gly Ile Asp Lys Asp Lys Val Asp Lys  
 195 200 205  
 Ser Ala Val Gly Phe Glu Tyr Gln Gly Lys Thr Glu Lys His Glu Ser  
 210 215 220  
 Gln Lys Asp Tyr Val Lys Gly Phe Gly Gly Lys Phe Gly Val Gln Thr  
 225 230 235 240  
 Asp Arg Gln Asp Lys Cys Ala Leu Gly Trp Asp His Gln Glu Lys Leu  
 245 250 255  
 Gln Leu His Glu Ser Gln Lys Asp Tyr Lys Thr Gly Phe Gly Gly Lys  
 260 265 270  
 Phe Gly Val Gln Ser Glu Arg Gln Asp Ser Ser Ala Val Gly Phe Asp  
 275 280 285  
 Tyr Lys Glu Arg Leu Ala Lys His Glu Pro Gln Gln Asp Tyr Ala Lys  
 290 295 300  
 Gly Phe Gly Gly Lys Tyr Gly Val Gln Lys Asp Arg Met Asp Lys Asn  
 305 310 315 320  
 Ala Ser Thr Phe Glu Glu Val Val Gln Val Pro Ser Ala Tyr Gln Lys  
 325 330 335  
 Thr Val Pro Ile Glu Ala Val Thr Ser Lys Thr Ser Asn Ile Arg Ala  
 340 345 350  
 Asn Phe Glu Asn Leu Ala Lys Glu Arg Glu Gln Glu Asp Arg Arg Lys  
 355 360 365  
 Ala Glu Ala Glu Arg Ala Gln Arg Met Ala Lys Glu Arg Gln Glu Gln

|         |                             |                         |                             |         |
|---------|-----------------------------|-------------------------|-----------------------------|---------|
| 370     |                             | 375                     |                             | 380     |
| Glu 385 | Glu Ala Arg Arg Lys 390     | Leu Glu Glu Gln Ala 395 | Arg Ala Lys Lys Gln 400     |         |
| Thr     | Pro Pro Ala Ser 405         | Pro Ser Pro Gln 410     | Ile Glu Asp Arg Pro 415     | Pro     |
| Ser     | Ser Pro Ile 420             | Tyr Glu Asp Ala 425     | Pro Phe Lys Ala Glu 430     | Pro Ser |
| Tyr     | Arg Gly Ser Glu Pro Glu 435 | Pro Glu Tyr Ser Ile 440 | Glu Ala Ala Gly 445         |         |
| Ile     | Pro Glu Ala Gly Ser 450     | Gln Gln Gly Leu Thr 455 | Tyr Thr Ser Glu Pro 460     |         |
| Val 465 | Tyr Glu Thr Thr Glu 470     | Ala Pro Gly His Tyr 475 | Gln Ala Glu Asp Asp 480     |         |
| Thr     | Tyr Asp Gly Tyr 485         | Glu Ser Asp Leu Gly 490 | Ile Thr Ala Ile Ala 495     | Leu     |
| Tyr     | Asp Tyr Gln 500             | Ala Ala Gly Asp 505     | Asp Glu Ile Ser Phe Asp 510 | Pro Asp |
| Asp     | Ile Ile Thr Asn Ile Glu 515 | Met Ile Asp Asp Gly 520 | Trp Trp Arg Gly 525         |         |
| Val     | Cys Lys Gly Arg Tyr Gly 530 | Leu Phe Pro Ala Asn 535 | Tyr Val Glu Leu 540         |         |
| Arg 545 | Gln                         |                         |                             |         |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAGCAGTCCT TCACCATGGT GGCCGACACT CCGGAAAACC TCCGCCTCAA GCAACAGAGC | 60  |
| GAGCTGCAGA GTCAGGTGCG CTACAAGGAG GAGTTTGAGA AGAATAAGGG CAAAGGTTTC | 120 |
| AGCGTGGTGG CAGACACGCC TGAGCTGCAG AGAATCAAGA AGACCCAGGA CCAGATCAGC | 180 |
| AATATCAAAT ACCATGAGGA GTTTGAGAAG AGCCGCATGG GGCCCAGTGG AGGAGAAGGG | 240 |
| GTGGAACCAG AGCGCCGAGA AGCCCAGGAC AGCAGCAGCT ACCGGAGGCC CACAGAGCAG | 300 |
| CAGCAGCCGC AGCCTCACCA TATCCCGACC AGTGCCCCCG TGTACCAGCA GCCCCAGCAG | 360 |
| CAGCAGATGA CCTCGTCCTA TGGTGGGTAC AAGGAGCCAG CAGCCCCTGT CTCCATACAG | 420 |
| CGCAGTGCCC CAGGTGGCGG TGGGAAACGG TACCGTGCG TGTATGACTA CAGCGCTGCC  | 480 |
| GACGAGGACG AGGTCTCCTT CCAGGATGGG GACACCATCG TCAATGTGCA CCAGATCGAT | 540 |
| GACGGCTGGA TGTACGGGAC CGTAGAGCGC ACCGGTGACA CGGGGATGCT GCCAGCCAAC | 600 |



|                                                                   |      |
|-------------------------------------------------------------------|------|
| TACGTGGAGG CCATCTGAAC CCTGTGCCGC CCCGCCCTGT CTTCAATGCA TTCCATGGCA | 660  |
| TCACATCTGT CCTGGGGCCT GACCCGTCCA CCCTTCAGTG TCTCTGTCTT TTAAGATCTT | 720  |
| CAACTGCTTC TTTATCCCCG CCCCTCCAGC TTATTTTACC ATCCCAAGCC TTGTTCTGCC | 780  |
| CCTGTCATGG GCTCCTTCCT CTGGCAGGTT TTCCCTTGGA CCAATCAACT GATTGATTTT | 840  |
| TCTCTCTGGA TGAACAGGC TGGGCACTCT GGGGAGGGCA GGATTGTTCT TAGCTAGGTA  | 900  |
| GACTCCAGG GCTGGGCTGA ACTAGGAGAC CCACTAAGGA GATCAGTTTA GACTGGGTGC  | 960  |
| AGTGGCAAAC ACCCTTAATT CCCAGCGAAG GGAGTCAGAG GCAGGCAGAT CTGTGACTTG | 1020 |
| GAAGCCAGCC TGGTCTACAT CGAGAGTTTC AGGACAGCCA GAGCTATGTA GTGAGGCCCT | 1080 |
| GTCTCGGAGG AAGAGTGGGG GTTGGTTAGC TCTCAGCTTC ACTTCCTGCC TTAGGCTCCT | 1140 |
| CAGAACCCCT GGCCCAGCTC CCCCAACTCC CTTCTCCTA GAGGTGGGGT GAGCTGTGC   | 1199 |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Ser | Phe | Thr | Met | Val | Ala | Asp | Thr | Pro | Glu | Asn | Leu | Arg | Leu | 1   | 5   | 10  | 15  |
| Lys | Gln | Gln | Ser | Glu | Leu | Gln | Ser | Gln | Val | Arg | Tyr | Lys | Glu | Glu | Phe | 20  | 25  | 30  |     |
| Glu | Lys | Asn | Lys | Gly | Lys | Gly | Phe | Ser | Val | Val | Ala | Asp | Thr | Pro | Glu | 35  | 40  | 45  |     |
| Leu | Gln | Arg | Ile | Lys | Lys | Thr | Gln | Asp | Gln | Ile | Ser | Asn | Ile | Lys | Tyr | 50  | 55  | 60  |     |
| His | Glu | Glu | Phe | Glu | Lys | Ser | Arg | Met | Gly | Pro | Ser | Gly | Gly | Glu | Gly | 65  | 70  | 75  | 80  |
| Val | Glu | Pro | Glu | Arg | Arg | Glu | Ala | Gln | Asp | Ser | Ser | Ser | Tyr | Arg | Arg | 85  | 90  | 95  |     |
| Pro | Thr | Glu | Gln | Gln | Gln | Pro | Gln | Pro | His | His | Ile | Pro | Thr | Ser | Ala | 100 | 105 | 110 |     |
| Pro | Val | Tyr | Gln | Gln | Pro | Gln | Gln | Gln | Met | Thr | Ser | Ser | Tyr | Gly |     | 115 | 120 | 125 |     |
| Gly | Tyr | Lys | Glu | Pro | Ala | Ala | Pro | Val | Ser | Ile | Gln | Arg | Ser | Ala | Pro | 130 | 135 | 140 |     |
| Gly | Gly | Gly | Gly | Lys | Arg | Tyr | Arg | Ala | Val | Tyr | Asp | Tyr | Ser | Ala | Ala | 145 | 150 | 155 | 160 |
| Asp | Glu | Asp | Glu | Val | Ser | Phe | Gln | Asp | Gly | Asp | Thr | Ile | Val | Asn | Val | 165 | 170 | 175 |     |
| Gln | Gln | Ile | Asp | Asp | Gly | Trp | Met | Tyr | Gly | Thr | Val | Glu | Arg | Thr | Gly |     |     |     |     |

Asp Thr Gly Met Leu Pro Ala Asn Tyr Val Glu Ala Ile  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATGGCGGTGA ACCTGAGCCG GAACGGGCCG GCGCTGCAGG AGGCCTACGT GCGCGTAGTC  | 60   |
| ACCGAGAAAT CCCCAGACCGA CTGGGCTCTT TTTACCTATG AAGGCAACAG CAATGACATC | 120  |
| CGTGTGGCTG GCACAGGAGA GGGAGGCCTG GAGGAGCTGG TGGAAGAGCT CAACAGCGGG  | 180  |
| AAGGTGATGT ACGCCTTCTG CAGGGTGAAG GACCCCAACT CCGGCCTGCC CAAGTTTGTC  | 240  |
| CTCATCAACT GGACAGGAGA GGGTGTGAAT GATGTGCGGA AAGGAGCATG TGCCAACCAC  | 300  |
| GTCAGCACCA TGGCCAACTT CCTGAAGGGT GCCCACGTGA CCATCAATGC CCGGGCCGAG  | 360  |
| GAGGATGTGG AGCCTGAGTG CATCATGGAG AAGGTTGCCA AGGCCTCTGG GGCCAACTAC  | 420  |
| AGCTTCCATA AGGAAAGCAC CTCCTTCCAG GATGTAGGGC CGCAGGCCCC AGTGGGCTCT  | 480  |
| GTGTACCAGA AGACCAATGC CATATCTGAG ATCAAGAGAG TCGGCAAGGA TAACTTCTGG  | 540  |
| GCCAAAGCTG AGAAGGAAGA AGAGAACCGC CGCCTGGAGG AGAAGCGGCG TGCCGAAGAG  | 600  |
| GAGCGGCAGC GGTGAGGAGA GGAGCGACGA GAGCGGGAGC TGCAGGAGGC TGCCCGACGT  | 660  |
| GAGCAGCGCT ACCAGGAACA GCACAGATCA GCTGGAGCCC CGAGCAGGAC AGGTGAGCCA  | 720  |
| GAGCAGGAAG CCGTTTCAAG GACCAGACAG GAGTGGGAGT CTGCTGGGCA GCAGGCCCCA  | 780  |
| CACCCACGAG AGATTTTCAA GCAGAAGGAA AGGGCAATGT CCACCACCTC TGTCACCAGC  | 840  |
| TCGCAGCCGG GCAAGCTGAG GAGCCCCTTC CTGCAGAAGC AACTCACTCA ACCAGAAACC  | 900  |
| TCCTACGGCC GAGAGCCCAC AGCTCCTGTC TCCCGGCCTG CAGCAGGTGT CTGTGAGGAG  | 960  |
| CCAGCGCCTA GCACTCTGTC TTCTGCCCAG ACAGAAGAAG AACCTACATA TGAAGTACCC  | 1020 |
| CCAGAGCAGG ACACCCTCTA TGAGGAACCA CCACTGGTAC AGCAGCAAGG GGCTGGCTCC  | 1080 |
| GAACACATTG ACAACTACAT GCAGAGCCAG GGCTTCAGTG GACAAGGGCT GTGCGCCCGG  | 1140 |
| GCCTTGATG ACTACCAGGC AGCTGATGAC ACCGAGATCT CTTTGACCC TGAGAACCTA    | 1200 |
| ATCACAGGCA TCGAGGTGAT TGACGAAGGC TGGTGCGGAG GCTATGGGCC TGACGGCCAC  | 1260 |
| TTTGGCATGT TTCCTGCCAA CTACGTGGAG CTCATAGAGT GA                     | 1302 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Asn | Leu | Ser | Arg | Asn | Gly | Pro | Ala | Leu | Gln | Glu | Ala | Tyr | 1   | 5   | 10  | 15  |
| Val | Arg | Val | Val | Thr | Glu | Lys | Ser | Pro | Thr | Asp | Trp | Ala | Leu | Phe | Thr | 20  | 25  | 30  |     |
| Tyr | Glu | Gly | Asn | Ser | Asn | Asp | Ile | Arg | Val | Ala | Gly | Thr | Gly | Glu | Gly | 35  | 40  | 45  |     |
| Gly | Leu | Glu | Glu | Leu | Val | Glu | Glu | Leu | Asn | Ser | Gly | Lys | Val | Met | Tyr | 50  | 55  | 60  |     |
| Ala | Phe | Cys | Arg | Val | Lys | Asp | Pro | Asn | Ser | Gly | Leu | Pro | Lys | Phe | Val | 65  | 70  | 75  | 80  |
| Leu | Ile | Asn | Trp | Thr | Gly | Glu | Gly | Val | Asn | Asp | Val | Arg | Lys | Gly | Ala | 85  | 90  | 95  |     |
| Cys | Ala | Asn | His | Val | Ser | Thr | Met | Ala | Asn | Phe | Leu | Lys | Gly | Ala | His | 100 | 105 | 110 |     |
| Val | Thr | Ile | Asn | Ala | Arg | Ala | Glu | Glu | Asp | Val | Glu | Pro | Glu | Cys | Ile | 115 | 120 | 125 |     |
| Met | Glu | Lys | Val | Ala | Lys | Ala | Ser | Gly | Ala | Asn | Tyr | Ser | Phe | His | Lys | 130 | 135 | 140 |     |
| Glu | Ser | Thr | Ser | Phe | Gln | Asp | Val | Gly | Pro | Gln | Ala | Pro | Val | Gly | Ser | 145 | 150 | 155 | 160 |
| Val | Tyr | Gln | Lys | Thr | Asn | Ala | Ile | Ser | Glu | Ile | Lys | Arg | Val | Gly | Lys | 165 | 170 | 175 |     |
| Asp | Asn | Phe | Trp | Ala | Lys | Ala | Glu | Lys | Glu | Glu | Glu | Asn | Arg | Arg | Leu | 180 | 185 | 190 |     |
| Glu | Glu | Lys | Arg | Arg | Ala | Glu | Glu | Glu | Arg | Gln | Arg | Leu | Glu | Glu | Glu | 195 | 200 | 205 |     |
| Arg | Arg | Glu | Arg | Glu | Leu | Gln | Glu | Ala | Ala | Arg | Arg | Glu | Gln | Arg | Tyr | 210 | 215 | 220 |     |
| Gln | Glu | Gln | His | Arg | Ser | Ala | Gly | Ala | Pro | Ser | Arg | Thr | Gly | Glu | Pro | 225 | 230 | 235 | 240 |
| Glu | Gln | Glu | Ala | Val | Ser | Arg | Thr | Arg | Gln | Glu | Trp | Glu | Ser | Ala | Gly | 245 | 250 | 255 |     |
| Gln | Gln | Ala | Pro | His | Pro | Arg | Glu | Ile | Phe | Lys | Gln | Lys | Glu | Arg | Ala | 260 | 265 | 270 |     |
| Met | Ser | Thr | Thr | Ser | Val | Thr | Ser | Ser | Gln | Pro | Gly | Lys | Leu | Arg | Ser | 275 | 280 | 285 |     |
| Pro | Phe | Leu | Gln | Lys | Gln | Leu | Thr | Gln | Pro | Glu | Thr | Ser | Tyr | Gly | Arg | 290 | 295 | 300 |     |
| Glu | Pro | Thr | Ala | Pro | Val | Ser | Arg | Pro | Ala | Ala | Gly | Val | Cys | Glu | Glu | 305 | 310 | 315 | 320 |

Pro Ala Pro Ser Thr Leu Ser Ser Ala Gln Thr Glu Glu Glu Pro Thr  
 325 330 335  
 Tyr Glu Val Pro Pro Glu Gln Asp Thr Leu Tyr Glu Glu Pro Pro Leu  
 340 345 350  
 Val Gln Gln Gln Gly Ala Gly Ser Glu His Ile Asp Asn Tyr Met Gln  
 355 360 365  
 Ser Gln Gly Phe Ser Gly Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp  
 370 375 380  
 Tyr Gln Ala Ala Asp Asp Thr Glu Ile Ser Phe Asp Pro Glu Asn Leu  
 385 390 395 400  
 Ile Thr Gly Ile Glu Val Ile Asp Glu Gly Trp Trp Arg Gly Tyr Gly  
 405 410 415  
 Pro Asp Gly His Phe Gly Met Phe Pro Ala Asn Tyr Val Glu Leu Ile  
 420 425 430  
 Glu

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2074 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTNNCACTCA CCGTCCGTGG TNNNNSTMMC SGWYNKRNTK YRRKMSSKRW YKWKKCRRS    | 60  |
| GCGGCGCCGA CCTGCGCGCG GAGGAAAGAA GTCGGTTCGG CGGCGCCGGC GGAAACCGGA   | 120 |
| GTTTCGAGCGG GAGGCCTGAC GCGGCGAGGC GGCATGTCGG TGGCGGGGCT GAAGAAGCAG  | 180 |
| TTCTACAAGG CGAGCCAGCT GGTTCAGCGAG AAGGTTGGTG GGGCCGAAGG GACCAAACCTG | 240 |
| GATGATGACT TTAAAGATAT GGAAAAGAAG GTGGATGTCA CCAGCAAGGC CGTGGCAGAG   | 300 |
| GTGCTGGTCA GAACCATAGA ATATCTGCAG CCTAACCCAG CCTCGAGAGC CAAGCTGACT   | 360 |
| ATGCTGAACA CCGTATCCAA GATCCGGGGC CAAGTGAAGA ACCCTGGCTA CCCACAGTCA   | 420 |
| GAGGGTCTGT TGGGAGAGTG CATGGTTCGC CATGGCAAGG AACTAGGTGG AGAGTCCAAC   | 480 |
| TTCGGTGATG CCCTGCTAGA TGCAGGTGAG TCCATGAAGC GCCTGGCTGA GGTGAAGGAC   | 540 |
| TCACTGGACA TCGAGGTCAA GCAGAACTTC ATTGACCCAC TACAGAACCT GTGTGACAAG   | 600 |
| GATCTGAAGG AGATCCAGCA CCACCTGAAG AAATTGGAGG GCCGCCGCCT TGACTTTGAC   | 660 |
| TACAAGAAGA AGCGCCAGGG CAAGATCCCC GATGAGGAGC TGCGCCAGGC CCTAGAGAAG   | 720 |
| TTCGAGGAGT CCAAGGAGGT GCGGAGAGC AGTATGCACA ACCTCCTGGA GACTGATATA    | 780 |
| GAGCAGGTGA GCCAGCTCTC GGCCCTGGTG GATGCCCAGC TGGACTACCA CCGGCAGGCA   | 840 |
| GTGCAGATCC TGGAGGAGCT GGCTGACAAG CTGAAGCGCA GGGTTCGGGA AGCCTCCTCA   | 900 |
| CGCCCCAAGC GGGAGTTCAA GCCCCGGCCC CGGGAGCCCT TTGAGCTTGG AGAGCTGGAG   | 960 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CAGCCCAATG GGGGATTCCC CTGTGCCCCA GCACCTAAGA TCACAGCCTC CTCATCATTT | 1020 |
| AGATCGTCAG ACAAGCCCAT CAGGATGCCC AGCAAGAGCA TGCCACCCCT GGACCAGCCA | 1080 |
| AGCTGCAAGG CGCTTTATGA TTTTGAGCCA GAGAATGATG GCGAGCTGGG CTTCCGTGAG | 1140 |
| GGGGACCTCA TCACGCTTAC CAACCAGATC GACGAGAACT GGTATGAGGG GATGCTGCAC | 1200 |
| GGCCAATCAG GCTTCTTCCC ACTCAGCTAC GTGCAGGTGC TGGTGCCTCT GCCTCAGTGA | 1260 |
| CTGGGCCTTT ACACCGCTGC CAGTCACAGT GCAGCAGCAG TCTAATGCCA AGGTGCTCTA | 1320 |
| GAAACACTAA TGTTCCTCCA GGGGGGACTC CTCCCCACTC CCTCAGCCCT GGGGCCCCC  | 1380 |
| TATCCTAAGA CTCGGAAGG CCCACCCTGA GGTTCATTG CCTTCCTGGT GGTATCAGCT   | 1440 |
| TCCAGCTGTT TCAACCCTTC CCAGCCCGTT GCTGGCGATG GSCNNYGCC CCCTCTCTAG  | 1500 |
| GCTCTCTAGA GGCAGGCAGG TCCTTGAAT CCCAGCCTG CAAGCAGAGG CTGGCCAGCT   | 1560 |
| CCCCAGCTCA GCACACAGAG ACACCTGGCA CCTGCTGCTC ATGAAGAAGT GCACAAGGCA | 1620 |
| CAAATGTGTA CACTTCCCAT GGGACCACAG ACCCAGCTCA GCTCTGTTGA AGACCAAGCA | 1680 |
| CAAAGGCCTT GAAGAGTGGA CATTCCCAGG TCCCTGGCAC CTTCCCTTGA GCCAGCTCCA | 1740 |
| TTGCTACTTA TTCATGTGAC TGAAGCTGAC CACAGGCAGC TGGCAGGTCC TTTTTTCAAC | 1800 |
| CAGCAGGCTA GGCTGGCCAT AGACCCAGCT CTGCCTCACC CTGCCATGTT CCAGTAATGG | 1860 |
| AGGCCTCCAG CCTGGGCTCT ATTACATTCT TCTCTACAGC TGCCCCATAA CCCGTGGCTT | 1920 |
| ATCCCTGGCA CGTGGGGCCA CACCCACGC CCCCTGGATA GGCAACACTG TCCTGCTCCA  | 1980 |
| GCCTGTGCTG ANATGAACTG TACTCCTAAT TTTTTTTTAA AAAAAAGTA TTAAATNTCT  | 2040 |
| CTTTCTATAT AAAANAAAGN TGGCCCTANN NGGA                             | 2074 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Ala | Gly | Leu | Lys | Lys | Gln | Phe | Tyr | Lys | Ala | Ser | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ser | Glu | Lys | Val | Gly | Cys | Ala | Glu | Gly | Thr | Lys | Leu | Asp | Asp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Asp | Met | Glu | Lys | Lys | Val | Asp | Val | Thr | Ser | Lys | Ala | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Leu | Val | Arg | Thr | Ile | Glu | Tyr | Leu | Gln | Pro | Asn | Pro | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ala | Lys | Leu | Thr | Met | Leu | Asn | Thr | Val | Ser | Lys | Ile | Arg | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Lys | Asn | Pro | Gly | Tyr | Pro | Gln | Ser | Glu | Gly | Leu | Leu | Gly | Glu | Cys |

| 85  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Val | Arg | His | Gly | Lys | Glu | Leu | Gly | Gly | Glu | Ser | Asn | Phe | Gly | Asp |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Ala | Leu | Leu | Asp | Ala | Gly | Glu | Ser | Met | Lys | Arg | Leu | Ala | Glu | Val | Lys |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Asp | Ser | Leu | Asp | Ile | Glu | Val | Lys | Gln | Asn | Phe | Ile | Asp | Pro | Leu | Gln |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |
| Asn | Leu | Cys | Asp | Lys | Asp | Leu | Lys | Glu | Ile | Gln | His | His | Leu | Lys | Lys |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Leu | Glu | Gly | Arg | Arg | Leu | Asp | Phe | Asp | Tyr | Lys | Lys | Lys | Arg | Gln | Gly |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Lys | Ile | Pro | Asp | Glu | Glu | Leu | Arg | Gln | Ala | Leu | Glu | Lys | Phe | Glu | Glu |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Ser | Lys | Glu | Val | Ala | Glu | Thr | Ser | Met | His | Asn | Leu | Leu | Glu | Thr | Asp |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Ile | Glu | Gln | Val | Ser | Gln | Leu | Ser | Ala | Leu | Val | Asp | Ala | Gln | Leu | Asp |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Tyr | His | Arg | Gln | Ala | Val | Gln | Ile | Leu | Glu | Glu | Leu | Ala | Asp | Lys | Leu |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Lys | Arg | Arg | Val | Arg | Glu | Ala | Ser | Ser | Arg | Pro | Lys | Arg | Glu | Phe | Lys |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |
| Pro | Arg | Pro | Arg | Glu | Pro | Phe | Glu | Leu | Gly | Glu | Leu | Glu | Gln | Pro | Asn |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Gly | Gly | Phe | Pro | Cys | Ala | Pro | Ala | Pro | Lys | Ile | Thr | Ala | Ser | Ser | Ser |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Phe | Arg | Ser | Ser | Asp | Lys | Pro | Ile | Arg | Met | Pro | Ser | Lys | Ser | Met | Pro |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Pro | Leu | Asp | Gln | Pro | Ser | Cys | Lys | Ala | Leu | Tyr | Asp | Phe | Glu | Pro | Glu |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |
| Asn | Asp | Gly | Glu | Leu | Gly | Phe | Arg | Glu | Gly | Asp | Leu | Ile | Thr | Leu | Thr |  |  |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |
| Asn | Gln | Ile | Asp | Glu | Asn | Trp | Tyr | Glu | Gly | Met | Leu | His | Gly | Gln | Ser |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |
| Gly | Phe | Phe | Pro | Leu | Ser | Tyr | Val | Gln | Val | Leu | Val | Pro | Leu | Pro | Gln |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1531 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CCTCACTCGC TCTCCCCGCG CACGCTCCGT CTCCGTCAGT CCCCTGAGCT GTTCTAGTGC | 60   |
| GCGGCGTGGA GCCAGGGCTC AGGCTGGTGG AGCGGCCGGG GCTGGAGGCT GGGAGTGCGG | 120  |
| CGCGCACGGC CTCCCCGCGC CATTATCCGC GCTCGCTTCG GCGGAGGCCG GCGCCAGGAT | 180  |
| GGCAGAGATG GGGAGCAAGG GGGTGACGGC GGGGAAGATC GCCAGCAACG TACAGAAGAA | 240  |
| GCTGACCCGA GCGCAGGAGA AGGTCCTGCA GAAACTGGGG AAGGCGGACG AGACGAAGGA | 300  |
| CGAGCAGTTT GAGCAGTGTG TCCAGAACTT CAATAAGCAG CTGACAGAGG GTACCCGGCT | 360  |
| GCAGAACGAT CTTCGCACCT ATCTGCCTTC TGTAAAGCG ATGCACGAAG CCTCCAAGAA  | 420  |
| GCTGAGTGAG TGTCTTCAGG AGGTGTACGA GCCCGAGTGG CCTGGCAGGG ATGAAGCAAA | 480  |
| CAAGATTGCA GAGAACAATG ACCTACTCTG GATGGACTAC CACCAGAAGC TGGTGGACCA | 540  |
| GGCTCTGCTG ACCATGGACA CCTACCTAGG CCAGTTCCTT GATATCAAGT CGCGCATTGC | 600  |
| CAAGCGGGGG CGGAAGCTGG TGGACTATGA CAGTGCCCGG CACCACTATG AGTCTCTTCA | 660  |
| AACCGCCAAA AAGAAGGATG AAGCCAAAAT TGCCAAGGCA GAAGAGGAGC TCATCAAAGC | 720  |
| CCAGAAGGTG TTCGAGGAGA TGAACGTGGA TCTGCAGGAG GAGCTGCCAT CCCTGTGGAA | 780  |
| CAGCCGTGTA GGTCTCTATG TCAACACGTT CCAGAGCATC GCGGGTCTGG AGGAAAATT  | 840  |
| CCATAAAGAG ATGAGTAAGC TCAATCAGAA CCTCAATGAT GTCCTGGTCA GCCTAGAGAA | 900  |
| GCAGCACGGG AGCAACACCT TCACAGTCAA GGCCCAACCC AGTGACAATG CCCCTGAGAA | 960  |
| AGGGAACAAG AGCCCGTCAC CTCCTCCAGA TGGCTCCCCT GCTGCTACCC CTGAGATCAG | 1020 |
| AGTGAACCAT GAGCCAGAGC CGGCCAGTGG GGCCTCACCC GGGGCTACCA TCCCAAGTC  | 1080 |
| CCCATCTCAG CCAGCAGAGG CCTCCGAGGT GGTGGGTGGA GCCCAGGAGC CAGGGGAGAC | 1140 |
| AGCAGCCAGT GAAGCAACCT CCAGCTCTCT TCCGGCTGTG GTGGTGGAGA CCTTCTCCGC | 1200 |
| AACTGTGAAT GGGGCGGTGG AGGGCAGCGC TGGGACTGGA CGCTTGGAAC TGCCCCGGG  | 1260 |
| ATTCATGTTT AAGGTTCAAG CCCAGCATGA TTACACGGCC ACTGACACTG ATGAGCTGCA | 1320 |
| ACTCAAAGCT GGCGATGTGG TGTGGTGAT TCCTTTCCAG AACCCAGAGG AGCAGGATGA  | 1380 |
| AGGCTGGCTC ATGGGTGTGA AGGAGAGCGA CTGGAATCAG CACAAGGAAC TGGAGAAATG | 1440 |
| CCGCGGCGTC TTCCCGGAGA ATTTTACAGA GCGGGTACAG TGACGGAGGA GCCTTCCGGA | 1500 |
| GTGTGAAGAA CCTTTCCCCC AAAGATGTGT G                                | 1531 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Met | Gly | Ser | Lys | Gly | Val | Thr | Ala | Gly | Lys | Ile | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Asn Val Gln Lys Lys Leu Thr Arg Ala Gln Glu Lys Val Leu Gln Lys  
 20 25 30  
 Leu Gly Lys Ala Asp Glu Thr Lys Asp Glu Gln Phe Glu Gln Cys Val  
 35 40 45  
 Gln Asn Phe Asn Lys Gln Leu Thr Glu Gly Thr Arg Leu Gln Lys Asp  
 50 55 60  
 Leu Arg Thr Tyr Leu Ala Ser Val Lys Ala Met His Glu Ala Ser Lys  
 65 70 75 80  
 Lys Leu Ser Glu Cys Leu Gln Glu Val Tyr Glu Pro Glu Trp Pro Gly  
 85 90 95  
 Arg Asp Glu Ala Asn Lys Ile Ala Glu Asn Asn Asp Leu Leu Trp Met  
 100 105 110  
 Asp Tyr His Gln Lys Leu Val Asp Gln Ala Leu Leu Thr Met Asp Thr  
 115 120 125  
 Tyr Leu Gly Gln Phe Pro Asp Ile Lys Ser Arg Ile Ala Lys Arg Gly  
 130 135 140  
 Arg Lys Leu Val Asp Tyr Asp Ser Ala Arg His His Tyr Glu Ser Leu  
 145 150 155 160  
 Gln Thr Ala Lys Lys Lys Asp Glu Ala Lys Ile Ala Lys Ala Glu Glu  
 165 170 175  
 Glu Leu Ile Lys Ala Gln Lys Val Phe Glu Glu Met Asn Val Asp Leu  
 180 185 190  
 Gln Glu Glu Leu Pro Ser Leu Trp Asn Ser Arg Val Gly Phe Tyr Val  
 195 200 205  
 Asn Thr Phe Gln Ser Ile Ala Gly Leu Glu Glu Asn Phe His Lys Glu  
 210 215 220  
 Met Ser Lys Leu Asn Gln Asn Leu Asn Asp Val Leu Val Ser Leu Glu  
 225 230 235 240  
 Lys Gln His Gly Ser Asn Thr Phe Thr Val Lys Ala Gln Pro Ser Asp  
 245 250 255  
 Asn Ala Pro Glu Lys Gly Asn Lys Ser Pro Ser Pro Pro Pro Asp Gly  
 260 265 270  
 Ser Pro Ala Ala Thr Pro Glu Ile Arg Val Asn His Glu Pro Glu Pro  
 275 280 285  
 Ala Ser Gly Ala Ser Pro Gly Ala Thr Ile Pro Lys Ser Pro Ser Gln  
 290 295 300  
 Pro Ala Glu Ala Ser Glu Val Val Gly Gly Ala Gln Glu Pro Gly Glu  
 305 310 315 320  
 Thr Ala Ala Ser Glu Ala Thr Ser Ser Ser Leu Pro Ala Val Val Val  
 325 330 335  
 Glu Thr Phe Ser Ala Thr Val Asn Gly Ala Val Glu Gly Ser Ala Gly  
 340 345 350  
 Thr Gly Arg Leu Asp Leu Pro Pro Gly Phe Met Phe Lys Val Gln Ala  
 355 360 365  
 Gln His Asp Tyr Thr Ala Thr Asp Thr Asp Glu Leu Gln Leu Lys Ala



|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 370                                                             |     | 375 |     | 380 |
| Gly Asp Val Val Leu Val Ile Pro Phe Gln Asn Pro Glu Glu Gln Asp |     |     |     |     |
| 385                                                             |     | 390 | 395 | 400 |
| Glu Gly Trp Leu Met Gly Val Lys Glu Ser Asp Trp Asn Gln His Lys |     |     |     |     |
|                                                                 | 405 |     | 410 | 415 |
| Glu Leu Glu Lys Cys Arg Gly Val Phe Pro Glu Asn Phe Thr Glu Arg |     |     |     |     |
|                                                                 | 420 | 425 |     | 430 |
| Val Gln                                                         |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GAATTCGTCG ACCCACGCGT CCGGTTTGAG CAGTGCCTCC AGAATTTCAA CAAGCAGCTG | 60   |
| ACGGAGGGCA CCCGGCTGCA GAAGGATCTC CGGACCTACC TGGCCTCCGT CAAAGCCATG | 120  |
| CACGAGGCTT CCAAGAAGCT GAATGAGTGT CTGCAGGAGG TGTATGAGCC CGATTGGCCC | 180  |
| GGCAGGGATG AGGCAAACAA GATCGCAGAG AACACGACC TGCTGTGGAT GGATTACCAC  | 240  |
| CAGAAGCTGG TGGACCAGGC GCTGCTGACC ATGGACACGT ACCTGGGCCA GTTCCCCGAC | 300  |
| ATCAAGTCAC GCATTGCCAA GCGGGGGCGC AAGCTGGTGG ACTACGACAG TGCCCGGCAC | 360  |
| CACTACGAGT CCCTTCAAAC TGCCAAAAAG AAGGATGAAG CCAAATTCG CAAGGCCGAG  | 420  |
| GAGGAGCTCA TCAAAGCCCA GAAGGTGTTT GAGGAGATGA ATGTGGATCT GCAGGAGGAG | 480  |
| CTGCCGTCCT TGTGGAACAG CCGCGTAGGT TTCTACGTCA ACACGTTCCA GAGCATCGCG | 540  |
| GGCCTGGAGG AAAACTTCCA CAAGGAGATG AGCAAGCTCA ACCAGAACCT CAATGATGTG | 600  |
| CTGGTCGGCC TGGAGAAGCA ACACGGGAGC AACACCTCCA CGGTCAAGGC CCAGCCCAGT | 660  |
| GACAACGCGC CTGCAAAAGG GAACAAGAGC CCTTCGCCTC CAGATGGCTC CCCTGCCGCC | 720  |
| ACCCCCGAGA TCAGAGTCAA CCACGAGCCA GAGCCGGCCG GCGGGGCCAC GCCCGGGGCC | 780  |
| ACCCTCCCCA AGTCCCCATC TCAGCCAGCA GAGGCCTCGG AGGTGGCGGG TGGGACCCAA | 840  |
| CCTGCGGCTG GAGCCCAGGA GCCAGGGGAG ACGGCGGCAA GTGAAGCAGC CTCCAGCTCT | 900  |
| CTTCCTGCTG TCGTGGTGGG GACCTTCCCA GCAACTGTGA ATGGCACCGT GGAGGGCGGC | 960  |
| AGTGGGGCCG GGCGCTTGGA CCTGCCCCCA GGTTCATGT TCAAGGTACA GGCCAGCAC   | 1020 |
| GACTACACGG CCACTGACAC AGACGAGCTG CAGCTCAAGG CTGGTGATGT GGTGCTGGTG | 1080 |
| ATCCCCTTCC AGAACCCTGA AGAGCAGGAT GAAGGCTGGC TCATGGGCGT GAAGGAGAGC | 1140 |
| GACTGGAACC AGCACAAGGA GCTGGAGAAG TGCCGTGGCG TCTTCCCCGA GAACTTCACT | 1200 |

GAGAGGGTCC CATGACGGCG GGGCCCAGGC AGCCTCCGGG CGTGTGAAGA ACACCTCCTC 1260  
 CCGAAAAATG TGTGGTTCTT TTTTGTGTTT TGTTCGTT TTTTCATCTTT TGAAGAGCAA 1320  
 AGGGAAATCA AGAGGAGACC CCCAGGCAGA GGGGCGTTCT CCCAAAGATT AGGTCGTTTT 1380  
 CCAAAGAGCC GCGTCCCGGC AAGTCCGGCG GAATTCACCA GTGTCCTGAA GCTGCTGTGT 1440  
 CCTCTAGTTG AGTTCTGGCG CCCCTGCCTG TGCCCGCATG TGTGCCTGGC CGCAGGGCGG 1500  
 GGCTGGGGGC TGCCGAGCCA CCATGCTTGC CTGAAGCTTC GGCCGCGCCA CCCGGGCAAG 1560  
 GGTCTCTTTT TCCTGGCAGC TGCTGTGGGT GGGGCCCAGA CACCAGCCTA ACCTGGCTCT 1620  
 GCCCCGAGA CGGTCTGTGT GCTGTTTGA AATAAATCTT AGTGTTCAAA ACAAATGAA 1680  
 ACAAAAAAAA TGATAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGGGCGG CCGC 1734

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Phe Val Asp Pro Arg Val Arg Phe Glu Gln Cys Val Gln Asn Phe  
 1 5 10 15  
 Asn Lys Gln Leu Thr Glu Gly Thr Arg Leu Gln Lys Asp Leu Arg Thr  
 20 25 30  
 Tyr Leu Ala Ser Val Lys Ala Met His Glu Ala Ser Lys Lys Leu Asn  
 35 40 45  
 Glu Cys Leu Gln Glu Val Tyr Glu Pro Asp Trp Pro Gly Arg Asp Glu  
 50 55 60  
 Ala Asn Lys Ile Ala Glu Asn Asn Asp Leu Leu Trp Met Asp Tyr His  
 65 70 75 80  
 Gln Lys Leu Val Asp Gln Ala Leu Leu Thr Met Asp Thr Tyr Leu Gly  
 85 90 95  
 Gln Phe Pro Asp Ile Lys Ser Arg Ile Ala Lys Arg Gly Arg Lys Leu  
 100 105 110  
 Val Asp Tyr Asp Ser Ala Arg His His Tyr Glu Ser Leu Gln Thr Ala  
 115 120 125  
 Lys Lys Lys Asp Glu Ala Lys Ile Ala Lys Ala Glu Glu Glu Leu Ile  
 130 135 140  
 Lys Ala Gln Lys Val Phe Glu Glu Met Asn Val Asp Leu Gln Glu Glu  
 145 150 155 160  
 Leu Pro Ser Leu Trp Asn Ser Arg Val Gly Phe Tyr Val Asn Thr Phe  
 165 170 175  
 Gln Ser Ile Ala Gly Leu Glu Glu Asn Phe His Lys Glu Met Ser Lys  
 180 185 190

Leu Asn Gln Asn Leu Asn Asp Val Leu Val Gly Leu Glu Lys Gln His  
 195 200 205  
 Gly Ser Asn Thr Ser Thr Val Lys Ala Gln Pro Ser Asp Asn Ala Pro  
 210 215 220  
 Ala Lys Gly Asn Lys Ser Pro Ser Pro Pro Asp Gly Ser Pro Ala Ala  
 225 230 235 240  
 Thr Pro Glu Ile Arg Val Asn His Glu Pro Glu Pro Ala Gly Gly Ala  
 245 250 255  
 Thr Pro Gly Ala Thr Leu Pro Lys Ser Pro Ser Gln Pro Ala Glu Ala  
 260 265 270  
 Ser Glu Val Ala Gly Gly Thr Gln Pro Ala Ala Gly Ala Gln Glu Pro  
 275 280 285  
 Gly Glu Thr Ala Ala Ser Glu Ala Ala Ser Ser Ser Leu Pro Ala Val  
 290 295 300  
 Val Val Glu Thr Phe Pro Ala Thr Val Asn Gly Thr Val Glu Gly Gly  
 305 310 315 320  
 Ser Gly Ala Gly Arg Leu Asp Leu Pro Pro Gly Phe Met Phe Lys Val  
 325 330 335  
 Gln Ala Gln His Asp Tyr Thr Ala Thr Asp Thr Asp Glu Leu Gln Leu  
 340 345 350  
 Lys Ala Gly Asp Val Val Leu Val Ile Pro Phe Gln Asn Pro Glu Glu  
 355 360 365  
 Gln Asp Glu Gly Trp Leu Met Gly Val Lys Glu Ser Asp Trp Asn Gln  
 370 375 380  
 His Lys Glu Leu Glu Lys Cys Arg Gly Val Phe Pro Glu Asn Phe Thr  
 385 390 395 400  
 Glu Arg Val Pro

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2003 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAGCCGCTGG AGGGGGCGCC TGGTGTAGAT GTGAAAAGCC GTAACCAGGA ACCAGTAAAG | 60  |
| ATGTGGAAGT CTGTAGTGGG GCATGATGTA TCGGTTTCCG TGGAGACCCA GGGTGATGAC | 120 |
| TGGGATACAG ACCCTGACTT TGTGAATGAC ATCTCCGAGA AGGAGCAACG GTGGGGAGCC | 180 |
| AAGACCATTG AGGGCTCTGG ACGCACAGAG CACATCAACA TCCACCAGCT GAGGAACAAA | 240 |
| GTGTCAGAGG AGCAGGACAT CCTCAAGAAG AAGGAGCTGG AATCGGGGCC TAAGGCATCC | 300 |
| CATGGCTATG GCGGTCAGTT TGGAGTGGAG AGAGACCGGA TGGACAAGAG TGCCGTGGGC | 360 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CACGAGTATG TTGCTGATGT GGAGAAACAC TCATCTCAGA CTGATGCSGC CAGAGGCTTT | 420  |
| GGGGGCAAAT ATGGAGTTGA GAGGGACCGG GCAGACAAGT CAGCGGTGGG CTTTGACTAC | 480  |
| AAAGGAGAAG TGGAAAAGCA TGCATCTCAG AAAGATTACT CTCATGGCTT TGGTGGCCGC | 540  |
| TACGGGGTAG AGAAGGATAA ACGGGACAAA GCAGCCCTGG GATACGACTA CAAAGGAGAG | 600  |
| ACGGAGAAGC ACGAGTCTCA GAGAGATTAT GCCAAGGGCT TTGGTGGCCA ATATGGAATC | 660  |
| CAGAAAGACC GAGTGATATA GAGTGCTGTT GGCTTCAATG AAATGGAGGC CCAACACG   | 720  |
| GCGTATAAGA ACACAACACC CATAGAAGCT GCTTCCAGTG GTGCCCCTGG GCTGAAGGCA | 780  |
| AAATTTGAGT CCCTGGCTGA GGAGAAGAGG AAGCGAGAGG AAGAAGAGAA GGCACAGCAG | 840  |
| ATGGCCAGGC AGCAACAGGA GCGAAAGGCT GTGGTAAAGA TGAGCCGAGA AGTCCAGCAG | 900  |
| CCATCCATGC CTGTGGAAGA GCCAGCGGCA CCAGCCAGT TGCCCAAGAA GATCTCCTCA  | 960  |
| GAGGTCTGGC CTCCAGCAGA GAGTCACCTA CCGCCAGAGT CTCAGCCAGT GAGAAGCAGA | 1020 |
| AGGGAATACC CTGTGCCCTC TCTGCCACG AGGCAGTCTC CATTGCAGAA TCACTTGGAG  | 1080 |
| GACAACGAGG AGCCCCCAGC TCTGCCCTT AGGACCCAG AAGGCCTCCA GGTGGTGGAA   | 1140 |
| GAGCCAGTGT ACGAAGCAGC ACCCGAGCTG GAGCCGGAGC CAGAGCCTGA CTATGAGCCA | 1200 |
| GAGCCAGAGA CAGAGCCTGA CTATGAGGAT GTTGGGGAGT TAGATCGGCA GGATGAGGAT | 1260 |
| GCAGAGGGAG ACTATGAGGA TGTGCTGGAG CCCGANGACA CCCCTTCTCT GTCCTACCAA | 1320 |
| GCTGGACCCT CAGCTGGGGC TGGTGGTGGC GGGATCTCTG CTATAGCCCT GTATGATTAC | 1380 |
| CAAGGAGAGG GAAGCGATGA GCTTTCCTTT GATCCAGATG ACATCATCAC TGACATTGAG | 1440 |
| ATGGTGGATG AAGGCTGGTG GCGGGGCCAA TGCCGTGGCC ACTTTGGACT TTTCCCTGCA | 1500 |
| AACTATGTCA AGCTCCTCTA ATGACCAGCC CATTGTCTTC CGACTTCCCG AATTCGAAGC | 1560 |
| TGCTCTGCCT CCCTCTTCCC ACTCCATGGT ACTGCTGCAA GGACCTGGCT GAACATCATG | 1620 |
| AGATGCCTGA AGTTCTGGCA GTCTGTCTCC CGCCTCTTTA AGAGCTTTAG GTAGAATCGC | 1680 |
| TCCAGGTGGG GGTGGGGGTG GGGGTGGGAT CCCTCTGTCC CTCTGTCACC ACTCTTCCCT | 1740 |
| GAGGTAGCTC ATGAAATCAT CTTGCAGACC TGCCTCCTTC AGCCGCACCC CAGCTCTGCC | 1800 |
| AACCTTGCTC TAGAGTGCTG GGATTCCCTT GCCCCGACCC TGGGTGCCAG CCTAGAGGGG | 1860 |
| AGGCTCTCAC AGGGCTGCCT GATTGCCCCT GTTGTGCTTT TGCTCATTTT TCTTCCCTTA | 1920 |
| GCAGACAAAT TGGAACTGCC CTTCTGTTTA GTCCTAAAC TGAAAATAAA ATGAGACTGT  | 1980 |
| GGCTAAAAAA AAAAAAAAAA AAA                                         | 2003 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Trp Lys Ser Val Val Gly His Asp Val Ser Val Ser Val Glu Thr  
1 5 10 15  
Gln Gly Asp Asp Trp Asp Thr Asp Pro Asp Phe Val Asn Asp Ile Ser  
20 25 30  
Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg  
35 40 45  
Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu  
50 55 60  
His Asp Ile Leu Lys Lys Lys Glu Leu Glu Ser Gly Pro Lys Ala Ser  
65 70 75 80  
His Gly Tyr Gly Gly Gln Phe Gly Val Glu Arg Asp Arg Met Asp Lys  
85 90 95  
Ser Ala Val Gly His Glu Tyr Val Ala Asp Val Glu Lys His Ser Ser  
100 105 110  
Gln Thr Asp Ala Ala Arg Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg  
115 120 125  
Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val  
130 135 140  
Glu Lys His Ala Ser Gln Lys Asp Tyr Ser His Gly Phe Gly Gly Arg  
145 150 155 160  
Tyr Gly Val Glu Lys Asp Lys Arg Asp Lys Ala Ala Leu Gly Tyr Asp  
165 170 175  
Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys  
180 185 190  
Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser  
195 200 205  
Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys  
210 215 220  
Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala  
225 230 235 240  
Lys Phe Glu Ser Leu Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu Glu  
245 250 255  
Lys Ala Gln Gln Met Ala Arg Gln Gln Gln Glu Arg Lys Ala Val Val  
260 265 270  
Lys Met Ser Arg Glu Val Gln Gln Pro Ser Met Pro Val Glu Glu Pro  
275 280 285  
Ala Ala Pro Ala Gln Leu Pro Lys Lys Ile Ser Ser Glu Val Trp Pro  
290 295 300  
Pro Ala Glu Ser His Leu Pro Pro Glu Ser Gln Pro Val Arg Ser Arg  
305 310 315 320  
Arg Glu Tyr Pro Val Pro Ser Leu Pro Thr Arg Gln Ser Pro Leu Gln  
325 330 335  
Asn His Leu Glu Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr  
340 345 350

Pro Glu Gly Leu Gln Val Val Glu Glu Pro Val Tyr Glu Ala Ala Pro  
 355 360 365  
 Glu Leu Glu Pro Glu Pro Glu Pro Asp Tyr Glu Pro Glu Pro Glu Thr  
 370 375 380  
 Glu Pro Asp Tyr Glu Asp Val Gly Glu Leu Asp Arg Gln Asp Glu Asp  
 385 390 395 400  
 Ala Glu Gly Asp Tyr Glu Asp Val Leu Glu Pro Glu Asp Thr Pro Ser  
 405 410 415  
 Leu Ser Tyr Gln Ala Gly Pro Ser Ala Gly Ala Gly Gly Ala Gly Ile  
 420 425 430  
 Ser Ala Ile Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu  
 435 440 445  
 Ser Phe Asp Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu  
 450 455 460  
 Gly Trp Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala  
 465 470 475 480  
 Asn Tyr Val Lys Leu Leu  
 485

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1296 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGATCCCCGG AGCCGGTCCG CTGGGCGGGG CGCAGGGCTG GAGGGGCGCG CGTGCCGGCG  | 60  |
| GCGGCCCAGC GTGAAAGCGC GGAGGCGGCC ATGGCGGGCA ACTTCGACTC GGAGGAGCGG  | 120 |
| AGTAGCTGGT ACTGGGGCCG CCTGAGCCGG CAGGAGGCGG TGGCGCTATT GCAGGGCCAG  | 180 |
| CGGCACGGGG TGTTCTGGT GCGGGACTCG AGCACCAGCC CCGGGGACTA TGTGCTTAGC   | 240 |
| GTCTCCGAAA ACTCGCGCGT CTCCCACTAC ATCATCAACA GCAGCGGCCC GCGCCCTCCA  | 300 |
| GTGCCTCCGT CGCCCGCTCA GCCTCCGCCG GGAGTGAGTC CCTCCAGCCT CCGAATAGGA  | 360 |
| GATCAAGAAT TTGATTCAAT GCCTGCTTTA CTGGAATTCT ACAAATACA CTATTTGGAC   | 420 |
| ACTACAACAT TGATAGAACC AGTGGCCAGA TCAAGGCAGG GTAGTGGAGT GATTCTCAGG  | 480 |
| CAGGAGGAGG CAGAGTATGT GCGGGCCCTG TTTGACTTTA ATGGGAATGA TGAAGAAGAT  | 540 |
| CTTCCCTTTA AGAAAGGAGA CATCCTGAGA ATCCGGGATA AGCCTGAAGA GCAGTGGTGG  | 600 |
| AATGCAGAGG ACAGCGAAGG AAAGAGGGGG ATGATTCTCTG TCCCTTACGT GGAGAAGTAT | 660 |
| AGACCTGCCT CCGCCTCAGT ATCGGCTCTG ATTGGAGGTA ACCAGGAGGG TTCCCACCCA  | 720 |
| CAGCCACTGG GTGGGCGGGA GCCTGGGCCC TATGCCCAAC CCAGCGTCAA CACTCCGCTC  | 780 |
| CCTAACCTCC AGAATGGGCC CATTTATGCC AGGGTTATCC AGAAGCGAGT CCCTAATGCC  | 840 |

TACGACAAGA CAGCCTTGGC TTTGGAGGTC GGTGAGCTGG TAAAGGTTAC GAAGATTAAT 900  
 GTGAGTGGTC AGTGGGAAGG GGAGTGTAAT GGCAAACGAG GTCACCTCCC ATTCACACAT 960  
 GTCCGTCTGC TGGATCAACA GAATCCCGAT GAGGACTTCA GCTGAGTATA GCTCGACAGT 1020  
 TTGCTGACAG ATGGAACAAT CTGTTTTCCC CCAATTGCCA TCTATACAAT TTTCTTACAG 1080  
 GTGTCAAAGC AGTCTAGTTT ATATAAGCAT TCTGTTACCT GGGATCTTTT TTAAGACTGA 1140  
 ACTACTCCAT TCTCACTTGT ATTTACCATA TTCAGGGTAC GAAACCGGAG GGCTTATGTG 1200  
 GTTAACTTCT GAGTTGGCAG TTTTAGGTGG TAGTGGCCGT GCCTGTATGA GAAGACGTAA 1260  
 ATACATTGCC TCCTTTCTTT TGGGCAAAAC AGATCA 1296

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp Tyr Trp Gly  
 1 5 10 15  
 Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly Gln Arg His  
 20 25 30  
 Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly Asp Tyr Val  
 35 40 45  
 Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile Ile Asn Ser  
 50 55 60  
 Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln Pro Pro Pro  
 65 70 75 80  
 Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu Phe Asp Ser  
 85 90 95  
 Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu Asp Thr Thr  
 100 105 110  
 Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser Gly Val Ile  
 115 120 125  
 Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn  
 130 135 140  
 Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg  
 145 150 155 160  
 Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu  
 165 170 175  
 Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys Tyr Arg Pro  
 180 185 190  
 Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln Glu Gly Ser  
 195 200 205

His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr Ala Gln Pro  
 210 215 220  
 Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro Ile Tyr Ala  
 225 230 235 240  
 Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys Thr Ala Leu  
 245 250 255  
 Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile Asn Val Ser  
 260 265 270  
 Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His Phe Pro Phe  
 275 280 285  
 Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu Asp Phe Ser  
 290 295 300

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3345 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| CCTCACCINN | CCTGGTGTAG | GTACCGGATC | GAATTCAAGC  | GAAAAACAGA | GCGGGGCTGA | 60   |
| CTGTAGCGTG | GAGCGCGAGC | CGGGCTGGAC | GCGCGCAAGC  | CCTTGCCGGG | GACCCGCGAG | 120  |
| GCAAGCAGTC | TCCCTGTGGA | GCGTCGTCCT | CCATCCCTGT  | AAGCACCGTT | ACAGAGAATG | 180  |
| AAACAAGGGC | AGAAGTTACA | GAGCCCGTGA | GGCATCTTCA  | AATAGAAGAC | TGGAGACTAG | 240  |
| AAAAAGAATA | TTGCCAGGAG | TTGGCATCCA | TTGGAAGACC  | TTGAGATCCT | CTCAGCTCAG | 300  |
| AACTCCAGGA | CCGATGCATC | TTCCACCAC  | CTTGAAGCAC  | TGAGCCCTCC | AGAGCTGCAT | 360  |
| CTGGGAAGAC | TCGCCTGCCT | CCAGCATGAG | TTCTGAATGT  | GATGTTGGAA | GCTCTAAAGC | 420  |
| TGTGGTGAAT | GGCTTGGCAT | CTGGCAACCA | TGGACCAGAC  | AAAGACATGG | ACCCTACCAA | 480  |
| AATCTGCACT | GGGAAAGGAA | CAGTGAATCT | TCGGGCCTCG  | TCTTCCTACA | GGGGAACCCC | 540  |
| AAGCAGCAGC | CCTGTGAGCC | CCCAGGAATC | TCCGAAGCAT  | GAAAGCAAGT | CAGATGAATG | 600  |
| GAAACTTTCT | TCCAGTGCAG | ATACCAATGG | CAACGCCCAG  | CCCTCCCCAC | TTGCTGCCAA | 660  |
| GGGCTATAGA | AGTGTGCATC | CCAGCCTTTC | TGCTGACAAG  | CCCCAGGGCA | GTCCTTTACT | 720  |
| AAACGAAGTT | TCTTCTTCCC | ACATTGAAAC | CGATTCCCAA  | GACTTCCCTC | CAACAAGCAG | 780  |
| ACCTTCGTCT | GCCTACCCCT | CCACCACCAT | CGTCAACCCCT | ACCATGTGTC | TCCTGCAGCA | 840  |
| CAATCGAGAG | CAGCAAAGC  | GACTCAGTAG | TCTTTCAGAT  | CCTGCCTCAG | AGAGAAGAGC | 900  |
| GGGTGAGCAG | GACCCAGTAC | CAACCCAGC  | AGAACTCACT  | TCGCCCCGCA | GGGCTTCTGA | 960  |
| GAGAAGGGCA | AAGGATGCTA | GCAGACGGGT | GGTGAGGAGC  | GCACAGGACC | TGAGCGATGT | 1020 |
| GTCTACAGAT | GAAGTGGGCA | TTCCACTCCG | GAATACCGAG  | CGATCGAAAG | ACTGGTACAA | 1080 |



|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| AACTATGTTT  | AAACAGATCC | ACAAACTGAA | CAGAGATGAT | GATTCTGATG | TCCATTCCCC | 1140 |
| TCGATACTCC  | TTCTCTGATG | ACACAAAGTC | TCCCCTTTCT | GTGCCTCGCT | CAAAAAGTGA | 1200 |
| GATGAACTAC  | ATCGAAGGGG | AGAAAGTGGT | TAAGAGGTCC | GCCACACTCC | CCCTCCCAGC | 1260 |
| CCGCTCTTCC  | TCACTCAAGT | CCAGCCCAGG | AAGAAACGAC | TGGGAGCCCC | TAGATAAGAA | 1320 |
| AGTGGATACG  | AGAAAATACC | GAGCAGAGCC | CAAAAGCATT | TACGAATATC | AGCCGGGCAA | 1380 |
| GTCTTCGGTC  | CTGACCAATG | AGAAGATGAG | TCGGGATATA | AGCCCAGAAG | AGATAGATTT | 1440 |
| AAAGAATGAA  | CCTTGGTATA | AATTCTTTTC | GGAATTGGAG | TTTGGGAGAC | CGAGCTCAGC | 1500 |
| AGTCAGCCCC  | ACTCCAGACA | TTACGTCAGA | GCCTCCTGGA | TATATCTATT | CTTCCAACCT | 1560 |
| CCATGCAGTG  | AAGAGAGAAT | CGGACGGGAC | CCCCGGGGGT | CTCGCTAGCT | TGGAGAATGA | 1620 |
| GAGGCAGATC  | TATAAGAGTG | TCTTGAAGG  | TGGCGACATC | CCTCTTCAGG | GCCTCAGTGG | 1680 |
| GCTCAAGCGA  | CCTTCCAGCT | CAGCTTCCAC | TAAAGATTCA | GAGTCACCAA | GACATTTTAT | 1740 |
| ACCAGCTGAT  | TACTTGAGT  | CCACAGAAGA | ATTTATTCGG | AGACGGCACG | ATGATAAAGA | 1800 |
| GAAACTTTTA  | GCGGACCAGA | GACGACTTAA | GCGCGAGCAA | GAAGAGGCCG | ATATTGCAGC | 1860 |
| TCGCCGCCAC  | ACAGGTGTCA | TCCCGACTCA | TCATCAGTTT | ATCACTAATG | AGCGCTTTGG | 1920 |
| GGACCTCCTC  | AATATAGATG | ATACGGCCAA | AAGGAAATCT | GGGTTAGAGA | TGAGACCTGC | 1980 |
| TCGAGCCAAA  | TTTGACTTTA | AAGCCCAGAC | CCTGAAGGAG | CTGCCTCTGC | AGAAGGGAGA | 2040 |
| CGTTGTTTAC  | ATCTACAGAC | AGATTGACCA | GAAGTGGTAT | GAAGGTGAAC | ACCATGGCCG | 2100 |
| GGTGGGAATC  | TTCCCACGCA | CCTATATCGA | GCTTCTTCCT | CCAGCTGAGA | AGGCTCAGCC | 2160 |
| CAGAAAGTTG  | GCACCCGTAC | AAGTTTTGGA | ATATGGAGAA | GCCATTGCAA | AGTTTAACTT | 2220 |
| TAATGGAGAT  | ACACAAGTAG | AAATGTCTTT | CCGAAAGGGG | GAGAGGATCA | CGCTGCTCCG | 2280 |
| ACAGGTGGAT  | GAGAACTGGT | ATGAAGGGAG | GATTCCTGGG | ACATCTCGCC | AAGGCATTTT | 2340 |
| CCCTATCACC  | TATGTAGATG | TGCTTAAGAG | GCCATTGGTG | AAAACCCCTG | TGGATTACAT | 2400 |
| CGACCTGCCT  | TATTCTTCTT | CCCCAAGTCG | CAGTGCCACT | GTGAGCCCAC | AGGCTTCTCA | 2460 |
| TCATTCAATTG | AGCGCAGGAC | CTGATCTCAC | AGAATCTGAA | AAGAACTATG | TGCAACCTCA | 2520 |
| AGCCCAGCAG  | CGAAGAGTCA | CCCCAGACAG | GAGTCAGCCC | TCACTGGATT | TGTGTAGCTA | 2580 |
| CCAAGCGTTA  | TATAGTTATG | TGCCACAGAA | CGATGATGAG | TTGGAACCTC | GAGATGGAGA | 2640 |
| TATTGTTGAT  | GTCATGGAAA | AATGTGACGA | TGGATGGTTT | GTTGGCACTT | CGAGAAGGAC | 2700 |
| GAGGCAGTTT  | GGTACTTTTC | CAGGCAACTA | TGTAAAACCT | TTATATCTAT | AAGAAGACTA | 2760 |
| AAAAGCACAG  | AGATTATTTT | TTATCGGAGG | ATGAAGCATC | ATTCATGAAC | TGGTCTCTTT | 2820 |
| ATTTAAGTAC  | TGAGTCAGTA | AGAAAACTAA | TGCAGTTGGT | AAAGAAAGAA | TTCAAAGAAG | 2880 |
| GAACAGAGAA  | GTGTGTTTGA | AACCCATTGT | GTATCAGGGA | TTAACTATCT | GCTGAAGACA | 2940 |
| TCTGTATTTA  | CATGACTGCT | TCTGGGAGCT | GCTCTAGCCC | CCGCTGCTTG | GGGAATCTGA | 3000 |
| TCTGGAGCAT  | GTCCATGAGC | AACATTAGCC | AAAAAAAAAA | GCTTGGGCCC | TATTCTATAG | 3060 |
| TGTCACCTAA  | ATACTAGCTT | GATCCGGCTG | CTAACAAAGC | CCGAAAGGAA | GCTGAGTTGC | 3120 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| TGCTGCCACC GCTGAGCAAT AACTAGCATA ACCCCTTGGG GCCTCTAAAC GGGTCTTGAG   | 3180 |
| GGGTTTTTTTG GCTGAAAGGA GGAACATATAT CCGGATAACC TGGCGTAATA GCGAAGAGGC | 3240 |
| CCGCACCGAT CGCCCTTCCC AACAGTTGGG CAGCCTGAAT GGCGAATGGA CGCGCCCTGT   | 3300 |
| AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA GGGTG                   | 3345 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Glu | Cys | Asp | Val | Gly | Ser | Ser | Lys | Ala | Val | Val | Asn | Gly | 1   | 5   | 10  | 15  |
| Leu | Ala | Ser | Gly | Asn | His | Gly | Pro | Asp | Lys | Asp | Met | Asp | Pro | Thr | Lys | 20  | 25  | 30  |     |
| Ile | Cys | Thr | Gly | Lys | Gly | Thr | Val | Thr | Leu | Arg | Ala | Ser | Ser | Ser | Tyr | 35  | 40  | 45  |     |
| Arg | Gly | Thr | Pro | Ser | Ser | Ser | Pro | Val | Ser | Pro | Gln | Glu | Ser | Pro | Lys | 50  | 55  | 60  |     |
| His | Glu | Ser | Lys | Ser | Asp | Glu | Trp | Lys | Leu | Ser | Ser | Ser | Ala | Asp | Thr | 65  | 70  | 75  | 80  |
| Asn | Gly | Asn | Ala | Gln | Pro | Ser | Pro | Leu | Ala | Ala | Lys | Gly | Tyr | Arg | Ser | 85  | 90  | 95  |     |
| Val | His | Pro | Ser | Leu | Ser | Ala | Asp | Lys | Pro | Gln | Gly | Ser | Pro | Leu | Leu | 100 | 105 | 110 |     |
| Asn | Glu | Val | Ser | Ser | Ser | His | Ile | Glu | Thr | Asp | Ser | Gln | Asp | Phe | Pro | 115 | 120 | 125 |     |
| Pro | Thr | Ser | Arg | Pro | Ser | Ser | Ala | Tyr | Pro | Ser | Thr | Thr | Ile | Val | Asn | 130 | 135 | 140 |     |
| Pro | Thr | Ile | Val | Leu | Leu | Gln | His | Asn | Arg | Glu | Gln | Gln | Lys | Arg | Leu | 145 | 150 | 155 | 160 |
| Ser | Ser | Leu | Ser | Asp | Pro | Ala | Ser | Glu | Arg | Arg | Ala | Gly | Glu | Gln | Asp | 165 | 170 | 175 |     |
| Pro | Val | Pro | Thr | Pro | Ala | Glu | Leu | Thr | Ser | Pro | Gly | Arg | Ala | Ser | Glu | 180 | 185 | 190 |     |
| Arg | Arg | Ala | Lys | Asp | Ala | Ser | Arg | Arg | Val | Val | Arg | Ser | Ala | Gln | Asp | 195 | 200 | 205 |     |
| Leu | Ser | Asp | Val | Ser | Thr | Asp | Glu | Val | Gly | Ile | Pro | Leu | Arg | Asn | Thr | 210 | 215 | 220 |     |
| Glu | Arg | Ser | Lys | Asp | Trp | Tyr | Lys | Thr | Met | Phe | Lys | Gln | Ile | His | Lys | 225 | 230 | 235 | 240 |
| Leu | Asn | Arg | Asp | Asp | Asp | Ser | Asp | Val | His | Ser | Pro | Arg | Tyr | Ser | Phe |     |     |     |     |

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Lys Phe Asn Phe Asn Gly Asp Thr Gln Val Glu Met Ser Phe Arg Lys  
 610 615 620  
 Gly Glu Arg Ile Thr Leu Leu Arg Gln Val Asp Glu Asn Trp Tyr Glu  
 625 630 635 640  
 Gly Arg Ile Pro Gly Thr Ser Arg Gln Gly Ile Phe Pro Ile Thr Tyr  
 645 650 655  
 Val Asp Val Leu Lys Arg Pro Leu Val Lys Thr Pro Val Asp Tyr Ile  
 660 665 670  
 Asp Leu Pro Tyr Ser Ser Ser Pro Ser Arg Ser Ala Thr Val Ser Pro  
 675 680 685  
 Gln Ala Ser His His Ser Leu Ser Ala Gly Pro Asp Leu Thr Glu Ser  
 690 695 700  
 Glu Lys Asn Tyr Val Gln Pro Gln Ala Gln Gln Arg Arg Val Thr Pro  
 705 710 715 720  
 Asp Arg Ser Gln Pro Ser Leu Asp Leu Cys Ser Tyr Gln Ala Leu Tyr  
 725 730 735  
 Ser Tyr Val Pro Gln Asn Asp Asp Glu Leu Glu Leu Arg Asp Gly Asp  
 740 745 750  
 Ile Val Asp Val Met Glu Lys Cys Asp Asp Gly Trp Phe Val Gly Thr  
 755 760 765  
 Ser Arg Arg Thr Arg Gln Phe Gly Thr Phe Pro Gly Asn Tyr Val Lys  
 770 775 780  
 Pro Leu Tyr Leu  
 785

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTNNCACTCA CCGTCCTGGT GATGGTACCG GATCGAATTC AAGCGTGGCC GTGGCCGTGG  | 60  |
| GGCGCGCGGG GACCGCCCGG GGTGCCCCGCT CCGCTCAGCG TCCGGGCCGC GTGGTCCGGC | 120 |
| GGAGCCCCGA GACCACCCCC GGGCGGGGCG CCGCCGCGAT GTCGGTGGCT GGGCTCAAGA  | 180 |
| AGCAGTTCCA CAAAGCCAGC CAGCTGTTTA GTGAAAAAAT AAGTGGTGCC GAAGGAACGA  | 240 |
| AGCTAGATGA AGAATTTCTG AACATGGAAA AGAAAATAGA TATCACCAGT AAAGCTGTTG  | 300 |
| CAGAAATCCT TTCAAAGGCC ACAGAGTATC TCCAACCCAA TCCAGCATAC AGAGCTAAGC  | 360 |
| TAGGAATGCT GAACACTGTG TCGAAGCTCC GAGGGCAGGT GAAGGCCACC GGCTACCCAC  | 420 |
| AGACGGAAGG CTTGCTGGGG GACTGCATGC TGAAGTATGG CAAGGAGCTC GGAGAAGACT  | 480 |
| CTGCTTTTGG CAACTCGTTG GTAGATGTTG GTGAGGCCCT GAAACTCATG GCTGAGGTGA  | 540 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| AAGACTCTCT | GGATATTAAT | GTGAAGCAAA | CTTTTATTGA | CCCACTGCAG | CTACTGCAAG | 600  |
| ACAAAGATTT | AAAGGAGATC | GGGCACCACC | TGAGAAAGCT | GGAAGGCCGT | CGCCTGGATT | 660  |
| ATGATTATAA | AAAGCGGCGG | GTAGGTAAGA | TCCCCGAGGA | AGAAATCAGA | CAAGCAGTAG | 720  |
| AGAAGTTTGA | AGAGTCAAAG | GAGTTGGCCG | AAAGGAGCAT | GTTTAATTTT | TTAGAAAATG | 780  |
| ATGTAGAGCA | AGTGAGCCAG | CTGGCTGTGT | TTGTAGAGGC | GGCATTAGAC | TATCACAGGC | 840  |
| AGTCCACAGA | GATCCTCCAG | GAGCTGCAGA | GCAAGCTGGA | GTTGCGAATA | TCTCTTGCAT | 900  |
| CCAAAGTCCC | CAAGCGAGAA | TTCATGCCAA | AGCCTGTGAA | CATGAGTTCC | ACCGATGCCA | 960  |
| ATGGGGTCCG | ACCCAGCTCT | TCATCAAAGA | CACCAGGTAC | TGACACTCCC | GCGGACCAGC | 1020 |
| CCTGCTGTCT | TGGTCTCTAT | GACTTTGAGC | CAGAAAATGA | AGGAGAATTA | GGATTTAAAG | 1080 |
| AAGGGGACAT | CATTACATTA | ACCAATCAGA | TAGATGAAAA | CTGGTATGAA | GGGATGCTTC | 1140 |
| GTGGGGAATC | CGGCTTCTTC | CCCATTAAAT | ACGTGGAAGT | CATTGTGCCT | TTACCTCCGT | 1200 |
| AAATGTGTCT | TTTGGACCTA | ACTTCAGAAC | TGAAATGAAT | TGGCACCAGT | GCTCTCTCAG | 1260 |
| TGTGGTGTTC | TGTGACANCC | TCGCTCTCTG | GCCCCACTTA | TCACTTTTGT | ATGTGTGTTT | 1320 |
| TCTTTATAAT | GTATTTTGTA | TCAATTTAAT | TTGTATAACT | GATTTCTTTG | TCCTAACTCA | 1380 |
| TAAAAATAGT | TTTCTTCTTG | TTCTAAAAAG | TCATTGGTTA | AATGTATTTG | CTTCCTGTTG | 1440 |
| CTAAACGAG  | TAAATTGCGC | CCATTCGAAT | GGCCTGGGTA | GTCCTTGAAT | GCAGTGGGAA | 1500 |
| CGCACCTTTT | GCAGCCATGA | AAGCTAAAGG | TTTGTTCCT  | GACATTATTG | ATGGCCTCTG | 1560 |
| GTCTTTTCCT | GTTTTAAGCT | TACCTGTGAA | CAGCCCAATA | AACNTGACAC | ACTGTANAAT | 1620 |
| AANAAGGGTG | GCCCA      |            |            |            |            | 1636 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Ala | Gly | Leu | Lys | Lys | Gln | Phe | His | Lys | Ala | Ser | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ser | Glu | Lys | Ile | Ser | Gly | Ala | Glu | Gly | Thr | Lys | Leu | Asp | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Phe | Leu | Asn | Met | Glu | Lys | Lys | Ile | Asp | Ile | Thr | Ser | Lys | Ala | Val | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Leu | Ser | Lys | Ala | Thr | Glu | Tyr | Leu | Gln | Pro | Asn | Pro | Ala | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ala | Lys | Leu | Gly | Met | Leu | Asn | Thr | Val | Ser | Lys | Leu | Arg | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Lys | Ala | Thr | Gly | Tyr | Pro | Gln | Thr | Glu | Gly | Leu | Leu | Gly | Asp | Cys |



|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| CTCTCCTGCT | TCCGCAGCCT | GTGAGCAGCA | GGCCTGCTAA | CTGCAGATCC  | ACAACCGCAC | 180  |
| AGCTCGCTAC | AGGTGCACCA | TGTCTGGCTC | CTACGATGAG | GCCTCAGAGG  | AGATCACAGA | 240  |
| TAGCTTCTGG | GAGGTGGGGA | ACTACAAGCG | GACGGTGAAG | CGCATCGACG  | ATGGGCACCG | 300  |
| CCTGTGCAAC | GACCTCATGA | GCTGCGTGCA | GGAGCGCGCC | AAGATCGAGA  | AGGCATACGC | 360  |
| GCAGCAGCTC | ACCGACTGGG | CCAAGCGCTG | GCGCCAGCTC | ATCGAGAAAG  | GTCCTCAGTA | 420  |
| TGGCAGCCTG | GAGCGGGCGT | GGGGCGCCAT | GATGACAGAA | GCAGATAAGG  | TCAGCGAGCT | 480  |
| GCACCAGGAG | GTGAAGAACA | GCCTGCTGAA | TGAGGACCTG | GAGAAAAGTCA | AGAACTGGCA | 540  |
| GAAGGATGCC | TATCACAAGC | AGATCATGGG | TGGCTTCAAG | GAGACGAAAG  | AGGCCGAGGA | 600  |
| TGGCTTCCGA | AAGGCCCAGA | AGCCCTGGGC | TAAAAAGATG | AAGGAGCTAG  | AGGCGGCCAA | 660  |
| GAAGGCCTAT | CACTTGGCTT | GTAAGGAGGA | AAGGCTGGCC | ATGACCCGGG  | AGATGAACAG | 720  |
| TAAGACAGAG | CAGTCGGTCA | CCCCTGAACA | GCAGAAGAAA | CTTGTGGACA  | AAGTGGACAA | 780  |
| ATGCAGACAG | GATGTGCAAA | AGACTCAGGA | GAAGTATGAG | AAGGTCCTGG  | AAGATGTGGG | 840  |
| CAAGACCACA | CCACAGTACA | TGGAGGGCAT | GGAGCAGGTG | TTTGAGCAGT  | GCCAGCAGTT | 900  |
| TGAGGAGAAG | CGGCTGGTCT | TCCTGAAGGA | AGTCCTGCTG | GATATCAAAC  | GGCATCTCAA | 960  |
| CCTAGCGGAG | AACAGCAGCT | ACATGCATGT | CTACCGAGAA | CTGGAGCAGG  | CCATCCGGGG | 1020 |
| GGCCGATGCC | CAGGAGGACC | TCAGGTGGTT | CCGCAGCACC | AGTGGCCCCG  | GGATGCCCAT | 1080 |
| GAAGTGGCCG | CAGTTCGAGG | AGTGAACCC  | AGACCTCCCG | CACACCACTG  | CCAAGAAGGA | 1140 |
| GAAACAGCCT | AAGAAGGCAG | AGGGGGCCAC | CCTGAGCAAT | GCCACTGGGG  | CTGTAGAATC | 1200 |
| CACATCCCAG | GCTGGGGACC | GTGGCAGTGT | TAGCAGCTAT | GACCGAGGCC  | AAACATATGC | 1260 |
| CACCGAGTGG | TCAGACGATG | AGAGCGGAAA | CCCCTTCGGG | GGCAATGAGG  | CCAATGGTGG | 1320 |
| CGCCAACCCC | TTCGAGGATG | ATGCCAAGGG | AGTTCGTGTA | CGGGCACTCT  | ATGACTACGA | 1380 |
| CGGTCAGGAG | CAGGATGAGC | TCAGCTTCAA | GGCCGGAGAT | GAGCTCACCA  | AGCTCGGAGA | 1440 |
| GGAAGACGAA | CAGGGTTGGT | GCCGCGGGCG | GCTGGACAGC | GGACAGCTGG  | GCCTCTATCC | 1500 |
| TGCCAACTAC | GTTGAGGCTA | TATAGCTACC | TTGCCACCC  | GACTCCTCTC  | AGTCCTTGTC | 1560 |
| CACCGCCTTC | CACCCCTCCC | CTCCCCCTTG | CCATAGAGTT | CCAGACATAT  | TTTCCGATCA | 1620 |
| AGCTTTTATT | TTTTTAAAG  | TCAAAACAGA | ACAAAAAAA  | AAAAAAAAAA  | GAAGAAATAC | 1680 |
| GAAGAGACAG | CGTTTGCAGC | CTACCTGGAG | GCCGGGGGGG | AGGGGGCTTA  | GGGTGATGGC | 1740 |
| CTCCCCACA  | GCGTGGGCAA | GGATCTTGGG | ACTAACCCAA | TGTCACATCT  | GGTCTATAGA | 1800 |
| GTCCACCAAA | GAGTCTCCTG | AGTCTTGAGG | GAGATCTTCT | GGATCCTTCT  | ACCCTGTCTC | 1860 |
| GCTCTCCTAT | CCCACCACAG | CTGCCAGCAG | CTGCCCATGT | CACCTGAGCC  | TGGCTTCCTA | 1920 |
| AACTCTCCTG | TCCCCTCTCC | TGTCCCCCTT | CAACGCCCCC | TTCTCTTAAA  | GGGCCCCCAA | 1980 |
| TCTTTAGTCT | TCCACTCTGC | CCTGGGGGTG | CTTTTCTCTT | CCCAGCCCTG  | TCCAGTGAGG | 2040 |
| CTGGGGGAGA | AGGCTGCGGA | GGGGAGGGGA | GTGTCTCTTC | ACTCCCCCAG  | ACATGAAGGC | 2100 |
| AGGTGAGTGG | GAGGGAGTCA | TGGCCTCCCT | GGCATAACAG | AGAGGAAGAA  | GGAGAACAGA | 2160 |

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| CCATCTGACC  | AGGCTGTGCA | ACACTCCCAA  | TGCCAAGCCC  | ATTTGAGGGA | TGAAAACCCCT | 2220 |
| AGCTGGGCT   | GTGGGCAGAG | GGCTCCTCCT  | CAGAGCCAAT  | GAGCATTTGC | AGAGACCCCTA | 2280 |
| CCTGTCTCTT  | TAGTCCTTGG | CAATGGGCAA  | AGCCTCTTCC  | TTGGAAAGTC | CAGGGCAAAG  | 2340 |
| CCAGCAACAG  | TAGCAACCTC | CTCTCACTCT  | GGGGAGGAGG  | CATTGGCCAC | CCATCCCCCT  | 2400 |
| CCCTTCATGG  | TCATTCAGAA | ACGCCACAGC  | CCCTCCCATC  | CCCAATCACT | GTGTCAGCAT  | 2460 |
| CAGCCTTTGT  | GAAGACGGTC | TACAAGGCTC  | TCACCTGGCC  | AACCTAGGAG | ATTGAGGGGC  | 2520 |
| TCAGGAACCT  | AGGAGATTCA | GGGGCTTGGG  | GAACCTCCAC  | CTTGGCACTG | TAAGGGGAAG  | 2580 |
| CCAGCAGCTC  | AGGCTGGTGT | GAGGAAGGAA  | CTCTGGATGG  | TCACTGTAGC | TTTCTTCCTT  | 2640 |
| GACCTTTTAG  | TCCCCAACAT | CCCCTCTGAA  | TGCTGGCAGC  | ACCCCCACCC | CCACACACAC  | 2700 |
| ACTCCCATTT  | CTCTAAGCCC | GAGAGTCTTG  | AGTCTTCATT  | AAAGGATTCT | GGGTGTGGGA  | 2760 |
| GGGGACACAG  | GGCCTTGTGG | TTGGGAAGCA  | GGTGGCAGGC  | TCTCCCTTGG | GAGGATGGGG  | 2820 |
| TGGGAAACGA  | AACAGGTCAA | CCAAGACCTC  | TTACAGTGGA  | AAGTGGTCAG | AGGCTGTTTC  | 2880 |
| TTTGGACCTT  | TGGGAACACA | GATTTGAGAA  | AGTCTCATAT  | TCACAGCTGG | TGTCCGCTAG  | 2940 |
| GCCTCTGGCC  | TACGGACACC | CTCTGCCTTG  | TGAATCAGGT  | GACCTTTTGG | GCCTCCAGGG  | 3000 |
| AAAGAACAGG  | ACCACCATCC | ATGTTCTCCG  | CGTCCCTTTA  | GCTCTCTGCT | GCTTCTCCTG  | 3060 |
| ACACTCAGGT  | CATGGACCCA | AGCTTTGGGG  | TCCTGACCAC  | CGCCCCCCCC | CACCCCCCTT  | 3120 |
| CTCTTGACTA  | GGCTGCAGCA | GGGCCTTCTG  | TTGGGTCAGT  | CCTCCTCAGG | GCCAGGAGCA  | 3180 |
| GGAACCTTAGC | ACTCAAGAGA | CAGGGCTGTA  | AGCACCCACT  | TCCCTGTCAC | TGTTTGCCCT  | 3240 |
| TGGGGCTTCA  | GCTGCAGCCC | AGGTTGGGGC  | CTGGAGCCCT  | CAGAACCGGA | AGCAGGATTC  | 3300 |
| AAACCTCCCC  | TTCTCCACAG | CCCCCCTGTC  | CTCCCCAGAT  | GGTAGACATC | CCCCAGCTCT  | 3360 |
| TACCTTCACC  | CTCATCTCAG | AAAGGCAAGA  | AGCCGCCATG  | TCCGCACCTT | GGGGCCTGGG  | 3420 |
| CTTCCCCCTC  | TCTGTGCCAG | CGGTTCCCAG  | CACCTGGGGA  | GGGGCTGTGG | CCTGACCAGA  | 3480 |
| CCCCAGGCCC  | ACCCACATA  | GTATACTAGC  | TGCCCCACTCT | GGGGCAGGAA | CTGGAAAATC  | 3540 |
| CATCCCTTTT  | GAACAACCAC | CTTCAATGAC  | CCCCCCCATC  | TGGGACCAGA | CTTGGTCTCTC | 3600 |
| AAGTTATTCA  | GCACCCCCAG | TGCAGGAGGG  | TCCTCCCCCC  | ACCCCCCGAA | GTCCCTGGAG  | 3660 |
| CCCGGAGCAG  | AGCCCCACCT | GTGATTCCCTG | GTGTTAGGGC  | ACCTCAAACC | TTGGGCTGGA  | 3720 |
| CCACACCCTT  | TCCCGCCATT | TCCAGACCCC  | TACCTGTACT  | CCCCAGTGCT | CCCCAGGGGC  | 3780 |
| CTCTTGATGC  | TGCACGGGAC | CCTGCAGGGC  | TCGGTCAGTG  | ATGTGTTTTG | TCCCCAGTTA  | 3840 |
| ACCGCCATCC  | AGCGACCTGG | TTCCAGGAGG  | AGCTCAGGTC  | ACCCCCACCA | CCGCCGCCAC  | 3900 |
| TGCGTCTGCC  | GCCCTAGGCT | TTCAGACATC  | ATTAGTTCCG  | ACACTTGTGA | AACTCCGAGA  | 3960 |
| CGTGCCGTGG  | TCTCAGCAAT | GCACCTGTTT  | TATACATGAT  | TGTGTAATTT | AAAGGTATAT  | 4020 |
| AAATACAAAT  | ATATATATTA | TATCTATATC  | TATCAGTTGT  | GACCGTATGG | CTGTCGATAA  | 4080 |
| AACCAGAATT  | C          |             |             |            |             | 4091 |



(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Gly Ser Tyr Asp Glu Ala Ser Glu Glu Ile Thr Asp Ser Phe  
1 5 10 15  
Trp Glu Val Gly Asn Tyr Lys Arg Thr Val Lys Arg Ile Asp Asp Gly  
20 25 30  
His Arg Leu Cys Asn Asp Leu Met Ser Cys Val Gln Glu Arg Ala Lys  
35 40 45  
Ile Glu Lys Ala Tyr Ala Gln Gln Leu Thr Asp Trp Ala Lys Arg Trp  
50 55 60  
Arg Gln Leu Ile Glu Lys Gly Pro Gln Tyr Gly Ser Leu Glu Arg Ala  
65 70 75 80  
Trp Gly Ala Met Met Thr Glu Ala Asp Lys Val Ser Glu Leu His Gln  
85 90 95  
Glu Val Lys Asn Ser Leu Leu Asn Glu Asp Leu Glu Lys Val Lys Asn  
100 105 110  
Trp Gln Lys Asp Ala Tyr His Lys Gln Ile Met Gly Gly Phe Lys Glu  
115 120 125  
Thr Lys Glu Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro Trp Ala  
130 135 140  
Lys Lys Met Lys Glu Leu Glu Ala Ala Lys Lys Ala Tyr His Leu Ala  
145 150 155 160  
Cys Lys Glu Glu Arg Leu Ala Met Thr Arg Glu Met Asn Ser Lys Thr  
165 170 175  
Glu Gln Ser Val Thr Pro Glu Gln Gln Lys Lys Leu Val Asp Lys Val  
180 185 190  
Asp Lys Cys Arg Gln Asp Val Gln Lys Thr Gln Glu Lys Tyr Glu Lys  
195 200 205  
Val Leu Glu Asp Val Gly Lys Thr Thr Pro Gln Tyr Met Glu Gly Met  
210 215 220  
Glu Gln Val Phe Glu Gln Cys Gln Gln Phe Glu Glu Lys Arg Leu Val  
225 230 235 240  
Phe Leu Lys Glu Val Leu Leu Asp Ile Lys Arg His Leu Asn Leu Ala  
245 250 255  
Glu Asn Ser Ser Tyr Met His Val Tyr Arg Glu Leu Glu Gln Ala Ile  
260 265 270  
Arg Gly Ala Asp Ala Gln Glu Asp Leu Arg Trp Phe Arg Ser Thr Ser  
275 280 285  
Gly Pro Gly Met Pro Met Asn Trp Pro Gln Phe Glu Glu Trp Asn Pro

|                                                                 |     |             |
|-----------------------------------------------------------------|-----|-------------|
| 290                                                             | 295 | 300         |
| Asp Leu Pro His Thr Thr Ala Lys Lys Glu Lys Gln Pro Lys Lys Ala |     |             |
| 305                                                             | 310 | 315 320     |
| Glu Gly Ala Thr Leu Ser Asn Ala Thr Gly Ala Val Glu Ser Thr Ser |     |             |
|                                                                 | 325 | 330 335     |
| Gln Ala Gly Asp Arg Gly Ser Val Ser Ser Tyr Asp Arg Gly Gln Thr |     |             |
|                                                                 | 340 | 345 350     |
| Tyr Ala Thr Glu Trp Ser Asp Asp Glu Ser Gly Asn Pro Phe Gly Gly |     |             |
|                                                                 | 355 | 360 365     |
| Asn Glu Ala Asn Gly Gly Ala Asn Pro Phe Glu Asp Asp Ala Lys Gly |     |             |
|                                                                 | 370 | 375 380     |
| Val Arg Val Arg Ala Leu Tyr Asp Tyr Asp Gly Gln Glu Gln Asp Glu |     |             |
|                                                                 | 385 | 390 395 400 |
| Leu Ser Phe Lys Ala Gly Asp Glu Leu Thr Lys Leu Gly Glu Glu Asp |     |             |
|                                                                 | 405 | 410 415     |
| Glu Gln Gly Trp Cys Arg Gly Arg Leu Asp Ser Gly Gln Leu Gly Leu |     |             |
|                                                                 | 420 | 425 430     |
| Tyr Pro Ala Asn Tyr Val Glu Ala Ile                             |     |             |
|                                                                 | 435 | 440         |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GAATTCGTCG ACCCACGGTC CGGGAAGCCT TTCACAAGCA GATGATGGGC GGCTTCAAGG  | 60  |
| AGACCAAGGA AGCTGAGGAC GGCTTTCGGA AGGCACAGAA GCCCTGGGCC AAGAAGCTGA  | 120 |
| AAGAGGTAGA AGCAGCAAAG AAAGCCCACC ATGCAGCGTG CAAAGAGGAG AAGCTGGCTA  | 180 |
| TCTCACGAGA AGCCAACAGC AAGGCAGACC CATCCCTCAA CCCTGAACAG CTAAGAAAT   | 240 |
| TGCAAGACAA AATAGAAAAG TGCAAGCAAG ATGTTCTTAA GACCAAAGAG AAGTATGAGA  | 300 |
| AGTCCCTGAA GGAACCTCGAC CAGGGCACAC CCCAGTACAT GGAGAACATG GAGCAGGTGT | 360 |
| TTGAGCAGTG CCAGCAGTTC GAGGAGAAAC GCCTTCGCTT CTTCCGGGAG GTTCTGCTGG  | 420 |
| AGGTTTCAGAA GCACCTAGAC CTGTCCAATG TGGCTGGTTA CAAAGCCATT TACCATGACC | 480 |
| TGGAGCAGAG CATCAGAGCA GCTGATGCAG TGGAGGACCT GAGGTGGTTC CGAGCCAATC  | 540 |
| ACGGGCCGGG CATGGCCATG AACTGGCCGC AGTTTGAGGA GTGGTCCGCA GACCTGAATC  | 600 |
| GAACCCTCAG CCGGAGAGAG AAGAAGAAGT CCACTGACGG CGTCACCCTG ACGGGCATCA  | 660 |
| ACCAGACAGG CGACAGTCT CTGCCGAGTA AGCCCAGCAG CACCCTTAAT GTCCCGAGCA   | 720 |
| ACCCCGCCCA GTCTGCGCAG TCACAGTCCA GCTACAACCC CTTGAGGAT GAGGACGACA   | 780 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CGGGCAGCAC CGTCAGTGAG AAGGACGACA CTAAGGCCAA AAATGTGAGC AGCTACGAGA | 840  |
| AGACCCAGAG CTATCCCACC GACTGGTCAG ACGATGAGTC TAACAACCCC TTCTCCTCCA | 900  |
| CGGATGCCAA TGGGGACTCG AATCCATTCG ACGACGACGC CACCTCGGGG ACGGAAGTGC | 960  |
| GAGTCCGGGC CCTGTATGAC TATGAGGGGC AGGAGCATGA TGAGCTGAGC TTCAAGGCTG | 1020 |
| GGGATGAGCT GACCAAGATG GAGGACGAGG ATGAGCAGGG CTGGTGCAAG GGACGCTTGG | 1080 |
| ACAACGGGCA AGTTGGCCTA TACCCGGCAA ATTATGTGGA GGCGATCCAG TGA        | 1133 |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Arg | Arg | Pro | Thr | Val | Arg | Glu | Ala | Phe | His | Lys | Gln | Met | Met | 1   | 5   | 10  | 15  |
| Gly | Gly | Phe | Lys | Glu | Thr | Lys | Glu | Ala | Glu | Asp | Gly | Phe | Arg | Lys | Ala | 20  | 25  | 30  |     |
| Gln | Lys | Pro | Trp | Ala | Lys | Lys | Leu | Lys | Glu | Val | Glu | Ala | Ala | Lys | Lys | 35  | 40  | 45  |     |
| Ala | His | His | Ala | Ala | Cys | Lys | Glu | Glu | Lys | Leu | Ala | Ile | Ser | Arg | Glu | 50  | 55  | 60  |     |
| Ala | Asn | Ser | Lys | Ala | Asp | Pro | Ser | Leu | Asn | Pro | Glu | Gln | Leu | Lys | Lys | 65  | 70  | 75  | 80  |
| Leu | Gln | Asp | Lys | Ile | Glu | Lys | Cys | Lys | Gln | Asp | Val | Leu | Lys | Thr | Lys | 85  | 90  | 95  |     |
| Glu | Lys | Tyr | Glu | Lys | Ser | Leu | Lys | Glu | Leu | Asp | Gln | Gly | Thr | Pro | Gln | 100 | 105 | 110 |     |
| Tyr | Met | Glu | Asn | Met | Glu | Gln | Val | Phe | Glu | Gln | Cys | Gln | Gln | Phe | Glu | 115 | 120 | 125 |     |
| Glu | Lys | Arg | Leu | Arg | Phe | Phe | Arg | Glu | Val | Leu | Leu | Glu | Val | Gln | Lys | 130 | 135 | 140 |     |
| His | Leu | Asp | Leu | Ser | Asn | Val | Ala | Gly | Tyr | Lys | Ala | Ile | Tyr | His | Asp | 145 | 150 | 155 | 160 |
| Leu | Glu | Gln | Ser | Ile | Arg | Ala | Ala | Asp | Ala | Val | Glu | Asp | Leu | Arg | Trp | 165 | 170 | 175 |     |
| Phe | Arg | Ala | Asn | His | Gly | Pro | Gly | Met | Ala | Met | Asn | Trp | Pro | Gln | Phe | 180 | 185 | 190 |     |
| Glu | Glu | Trp | Ser | Ala | Asp | Leu | Asn | Arg | Thr | Leu | Ser | Arg | Arg | Glu | Lys | 195 | 200 | 205 |     |
| Lys | Lys | Ser | Thr | Asp | Gly | Val | Thr | Leu | Thr | Gly | Ile | Asn | Gln | Thr | Gly | 210 | 215 | 220 |     |

Asp Gln Ser Leu Pro Ser Lys Pro Ser Ser Thr Leu Asn Val Pro Ser  
 225 230 235 240  
 Asn Pro Ala Gln Ser Ala Gln Ser Gln Ser Ser Tyr Asn Pro Phe Glu  
 245 250 255  
 Asp Glu Asp Asp Thr Gly Ser Thr Val Ser Glu Lys Asp Asp Thr Lys  
 260 265 270  
 Ala Lys Asn Val Ser Ser Tyr Glu Lys Thr Gln Ser Tyr Pro Thr Asp  
 275 280 285  
 Trp Ser Asp Asp Glu Ser Asn Asn Pro Phe Ser Ser Thr Asp Ala Asn  
 290 295 300  
 Gly Asp Ser Asn Pro Phe Asp Asp Asp Ala Thr Ser Gly Thr Glu Val  
 305 310 315 320  
 Arg Val Arg Ala Leu Tyr Asp Tyr Glu Gly Gln Glu His Asp Glu Leu  
 325 330 335  
 Ser Phe Lys Ala Gly Asp Glu Leu Thr Lys Met Glu Asp Glu Asp Glu  
 340 345 350  
 Gln Gly Trp Cys Lys Gly Arg Leu Asp Asn Gly Gln Val Gly Leu Tyr  
 355 360 365  
 Pro Ala Asn Tyr Val Glu Ala Ile Gln  
 370 375

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Ala Ala Ala Gly Gly Gly Ala Gly Gly Ala Gly Ala Gly Thr Gly  
 1 5 10 15  
 Thr Cys Ala Ala Ala Ala Ala Gly Ala Ala Gly Gly Ala Thr Gly Gly  
 20 25 30  
 Cys Gly Ala Gly Gly Ala Ala Ala Ala Gly Gly Cys Ala Ala Ala  
 35 40 45  
 Cys Ala Gly Gly Ala Ala Gly Cys Ala Cys Ala Ala Gly Ala Cys Ala  
 50 55 60  
 Ala Gly Cys Thr Gly Gly Gly Thr Cys Gly Gly Cys Thr Thr Thr Thr  
 65 70 75 80  
 Cys Cys Ala Thr Cys Ala Ala Cys Ala Cys Cys Ala Ala Gly Ala Ala  
 85 90 95  
 Cys Cys Ala Gly Cys Thr Ala Ala Gly Cys Cys Ala Gly Cys Thr Gly  
 100 105 110  
 Thr Cys Cys Ala Gly Gly Cys Ala Cys Cys Cys Thr Gly Gly Thr Cys  
 115 120 125

Cys Ala Cys Thr Gly Cys Ala Gly Ala Ala Ala Ala Gly Gly Gly  
 130 135 140  
 Thr Cys Cys Ala Cys Thr Thr Ala Cys Cys Ala Thr Thr Thr Cys Thr  
 145 150 155 160  
 Gly Cys Ala Cys Ala Gly Gly Ala Ala Ala Ala Thr Gly Thr Ala Ala  
 165 170 175  
 Ala Ala Gly Thr Gly Gly Thr Gly Thr Ala Thr Thr Ala Cys Cys Gly  
 180 185 190  
 Gly Gly Cys Ala Cys Thr Gly Thr Ala Cys Cys Cys Cys Thr Thr Thr  
 195 200 205  
 Gly Ala Ala Thr Cys Cys Ala Gly Ala Ala Gly Cys Cys Ala Thr Gly  
 210 215 220  
 Ala Thr Gly Ala Ala Ala Thr Cys Ala Cys Thr Ala Thr Cys Cys Ala  
 225 230 235 240  
 Gly Cys Cys Ala Gly Gly Ala Gly Ala Cys Ala Thr Ala Gly Thr Cys  
 245 250 255  
 Ala Thr Gly Gly Thr Gly Gly Ala Thr Gly Ala Ala Ala Gly Cys Cys  
 260 265 270  
 Ala Ala Ala Cys Thr Gly Gly Ala Gly Ala Ala Cys Cys Cys Gly Gly  
 275 280 285  
 Cys Thr Gly Gly Cys Thr Thr Gly Gly Ala Gly Gly Ala Gly Ala Ala  
 290 295 300  
 Thr Thr Ala Ala Ala Ala Gly Gly Ala Ala Ala Gly Ala Cys Ala Gly  
 305 310 315 320  
 Gly Gly Thr Gly Gly Thr Thr Cys Cys Cys Thr Gly Cys Ala Ala Ala  
 325 330 335  
 Cys Thr Ala Thr Gly Cys Ala Gly Ala Gly Ala Ala Ala Ala Thr Cys  
 340 345 350  
 Cys Cys Ala Gly Ala Ala Ala Ala Thr Gly Ala Gly Gly Thr Thr Cys  
 355 360 365  
 Cys Cys Gly Cys Thr Cys Cys Ala Gly Thr Gly Ala Ala Ala Cys Cys  
 370 375 380  
 Ala Gly Thr Gly Ala Cys Thr Gly Ala Thr Thr Cys Ala Ala Cys Ala  
 385 390 395 400  
 Thr Cys Thr Gly Cys Cys Cys Cys Thr Gly Cys Cys Cys Cys Cys Ala  
 405 410 415  
 Ala Ala Cys Thr Gly Gly Cys Cys Thr Thr Gly Cys Gly Thr Gly Ala  
 420 425 430  
 Gly Ala Cys Cys Cys Cys Cys Gly Cys Cys Cys Cys Thr Thr Thr Gly  
 435 440 445  
 Gly Cys Ala Gly Thr Ala Ala Cys Cys Thr Cys Thr Thr Cys Ala Gly  
 450 455 460  
 Ala Gly Cys Cys Cys Thr Cys Cys Ala Cys Gly Ala Cys Cys Cys Cys  
 465 470 475 480  
 Thr Ala Ala Thr Ala Ala Cys Thr Gly Gly Gly Cys Cys Gly Ala Cys

| 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Cys | Ala | Gly | Cys | Thr | Cys | Cys | Ala | Cys | Gly | Thr | Gly | Gly | Cys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Cys | Cys | Ala | Cys | Cys | Ala | Gly | Cys | Ala | Cys | Gly | Ala | Ala | Thr | Gly | Ala |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Gly | Ala | Ala | Ala | Cys | Cys | Ala | Gly | Ala | Ala | Ala | Cys | Gly | Gly | Ala | Thr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ala | Ala | Cys | Thr | Gly | Gly | Gly | Ala | Thr | Gly | Cys | Ala | Thr | Gly | Gly | Gly |
| 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     |     | 560 |
| Cys | Ala | Gly | Cys | Cys | Cys | Ala | Gly | Cys | Cys | Cys | Thr | Cys | Thr | Cys | Thr |
|     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |     |
| Cys | Ala | Cys | Cys | Gly | Thr | Thr | Cys | Cys | Ala | Ala | Gly | Thr | Gly | Cys | Cys |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Gly | Gly | Cys | Cys | Ala | Gly | Thr | Thr | Ala | Ala | Gly | Gly | Cys | Ala | Gly | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Gly | Gly | Thr | Cys | Cys | Gly | Cys | Cys | Thr | Thr | Thr | Ala | Cys | Thr | Cys | Cys |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ala | Gly | Cys | Cys | Ala | Cys | Gly | Gly | Cys | Cys | Ala | Cys | Thr | Gly | Gly | Cys |
| 625 |     |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     | 640 |
| Thr | Cys | Cys | Thr | Cys | Cys | Cys | Cys | Gly | Thr | Cys | Thr | Cys | Cys | Thr | Gly |
|     |     |     | 645 |     |     |     |     | 650 |     |     |     |     |     | 655 |     |
| Thr | Gly | Cys | Thr | Ala | Gly | Gly | Cys | Cys | Ala | Gly | Gly | Gly | Thr | Gly | Ala |
|     |     |     | 660 |     |     |     | 665 |     |     |     |     |     | 670 |     |     |
| Ala | Ala | Ala | Gly | Gly | Thr | Gly | Gly | Ala | Gly | Gly | Gly | Gly | Cys | Thr | Ala |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Cys | Ala | Ala | Gly | Cys | Thr | Cys | Ala | Ala | Gly | Cys | Cys | Cys | Thr | Ala | Thr |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Ala | Thr | Cys | Cys | Thr | Thr | Gly | Gly | Ala | Gly | Ala | Gly | Cys | Cys | Ala | Ala |
| 705 |     |     |     |     | 710 |     |     |     | 715 |     |     |     |     |     | 720 |
| Ala | Ala | Ala | Ala | Gly | Ala | Cys | Ala | Ala | Cys | Cys | Ala | Cys | Thr | Thr | Ala |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Ala | Ala | Thr | Thr | Thr | Thr | Ala | Ala | Cys | Ala | Ala | Ala | Ala | Ala | Thr | Gly |
|     |     |     | 740 |     |     |     | 745 |     |     |     |     |     | 750 |     |     |
| Ala | Thr | Gly | Thr | Cys | Ala | Thr | Cys | Ala | Cys | Cys | Gly | Thr | Cys | Cys | Thr |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Gly | Gly | Ala | Ala | Cys | Ala | Gly | Cys | Ala | Ala | Gly | Ala | Cys | Ala | Thr | Gly |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Thr | Gly | Gly | Thr | Gly | Gly | Thr | Thr | Thr | Gly | Gly | Ala | Gly | Ala | Ala | Gly |
| 785 |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     |     | 800 |
| Thr | Thr | Cys | Ala | Ala | Gly | Gly | Thr | Cys | Ala | Gly | Ala | Ala | Gly | Gly | Gly |
|     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |     |
| Thr | Thr | Gly | Gly | Thr | Thr | Cys | Cys | Cys | Cys | Ala | Ala | Gly | Thr | Cys | Thr |
|     |     |     | 820 |     |     |     | 825 |     |     |     |     | 830 |     |     |     |
| Thr | Ala | Cys | Gly | Thr | Gly | Ala | Ala | Ala | Cys | Thr | Cys | Ala | Thr | Thr | Thr |
|     | 835 |     |     |     |     | 840 |     |     |     |     |     | 845 |     |     |     |

Cys Ala Gly Gly Gly Cys Cys Cys Ala Thr Ala Ala Gly Gly Ala Ala  
 850 855 860  
 Gly Thr Cys Thr Ala Cys Ala Ala Gly Cys Ala Thr Gly Gly Ala Thr  
 865 870 875 880  
 Thr Cys Thr Gly Gly Thr Thr Cys Thr Thr Cys Ala Gly Ala Gly Ala  
 885 890 895  
 Gly Thr Cys Cys Thr Gly Cys Thr Ala Gly Thr Cys Thr Ala Ala Ala  
 900 905 910  
 Gly Cys Gly Ala Gly Thr Ala Gly Cys Cys Thr Cys Thr Cys Cys Ala  
 915 920 925  
 Gly Cys Ala Gly Cys Cys Ala Ala Gly Cys Cys Gly Ala Gly Cys Cys  
 930 935 940  
 Ala Ala Gly Cys Cys Gly Gly Thr Cys Gly Thr Thr Thr Cys Gly Gly  
 945 950 955 960  
 Gly Ala Gly Ala Ala Gly Ala Ala Ala Thr Thr Gly Cys Cys Cys Ala  
 965 970 975  
 Gly Gly Thr Thr Ala Thr Thr Gly Cys Cys Thr Cys Ala Thr Ala Cys  
 980 985 990  
 Ala Cys Cys Gly Cys Cys Ala Cys Cys Gly Gly Cys Cys Cys Cys Gly  
 995 1000 1005  
 Ala Gly Cys Ala Gly Cys Thr Cys Ala Cys Thr Cys Thr Cys Gly Cys  
 1010 1015 1020  
 Cys Cys Cys Thr Gly Gly Thr Cys Ala Gly Cys Thr Gly Ala Thr Thr  
 1025 1030 1035 1040  
 Thr Thr Gly Ala Thr Cys Cys Gly Ala Ala Ala Ala Ala Ala Gly Ala  
 1045 1050 1055  
 Ala Cys Cys Cys Ala Gly Gly Thr Gly Gly Ala Thr Gly Gly Thr Gly  
 1060 1065 1070  
 Gly Gly Ala Ala Gly Gly Ala Gly Ala Gly Cys Thr Gly Cys Ala Ala  
 1075 1080 1085  
 Gly Cys Ala Cys Gly Thr Gly Gly Gly Ala Ala Ala Ala Ala Gly Cys  
 1090 1095 1100  
 Gly Cys Cys Ala Gly Ala Thr Ala Gly Gly Cys Thr Gly Gly Thr Thr  
 1105 1110 1115 1120  
 Cys Cys Cys Ala Gly Cys Thr Ala Ala Thr Thr Ala Thr Gly Thr Ala  
 1125 1130 1135  
 Ala Ala Gly Cys Thr Thr Cys Thr Ala Ala Gly Cys Cys Cys Thr Gly  
 1140 1145 1150  
 Gly Gly Ala Cys Gly Ala Gly Cys Ala Ala Ala Ala Thr Cys Ala Cys  
 1155 1160 1165  
 Thr Cys Cys Ala Ala Cys Ala Gly Ala Gly Cys Cys Ala Cys Cys Thr  
 1170 1175 1180  
 Ala Ala Gly Thr Cys Ala Ala Cys Ala Gly Cys Ala Thr Thr Ala Gly  
 1185 1190 1195 1200  
 Cys Gly Gly Cys Ala Gly Thr Gly Thr Gly Cys Cys Ala Gly Gly Thr

| 1205 |     |     |     |     |     |     |     |     |     | 1210 |     |     |     |     | 1215 |  |  |  |  |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|--|--|--|
| Gly  | Ala | Thr | Thr | Gly | Gly | Gly | Ala | Thr | Gly | Thr  | Ala | Cys | Gly | Ala | Cys  |  |  |  |  |
| 1220 |     |     |     |     |     |     |     |     |     | 1225 |     |     |     |     | 1230 |  |  |  |  |
| Thr  | Ala | Cys | Ala | Cys | Cys | Gly | Cys | Gly | Cys | Ala  | Gly | Ala | Ala | Thr | Gly  |  |  |  |  |
| 1235 |     |     |     |     |     |     |     |     |     | 1240 |     |     |     |     | 1245 |  |  |  |  |
| Ala  | Cys | Gly | Ala | Thr | Gly | Ala | Gly | Cys | Thr | Gly  | Gly | Cys | Cys | Thr | Thr  |  |  |  |  |
| 1250 |     |     |     |     |     |     |     |     |     | 1255 |     |     |     |     | 1260 |  |  |  |  |
| Cys  | Ala | Ala | Cys | Ala | Ala | Gly | Gly | Gly | Cys | Cys  | Ala | Gly | Ala | Thr | Cys  |  |  |  |  |
| 1265 |     |     |     |     |     |     |     |     |     | 1270 |     |     |     |     | 1275 |  |  |  |  |
| Ala  | Thr | Cys | Ala | Ala | Cys | Gly | Thr | Cys | Cys | Thr  | Cys | Ala | Ala | Cys | Ala  |  |  |  |  |
| 1285 |     |     |     |     |     |     |     |     |     | 1290 |     |     |     |     | 1295 |  |  |  |  |
| Ala  | Gly | Gly | Ala | Gly | Gly | Ala | Cys | Cys | Cys | Thr  | Gly | Ala | Cys | Thr | Gly  |  |  |  |  |
| 1300 |     |     |     |     |     |     |     |     |     | 1305 |     |     |     |     | 1310 |  |  |  |  |
| Gly  | Thr | Gly | Gly | Ala | Ala | Ala | Gly | Gly | Ala | Gly  | Ala | Ala | Gly | Thr | Cys  |  |  |  |  |
| 1315 |     |     |     |     |     |     |     |     |     | 1320 |     |     |     |     | 1325 |  |  |  |  |
| Ala  | Ala | Thr | Gly | Gly | Ala | Cys | Ala | Ala | Gly | Thr  | Gly | Gly | Gly | Gly | Cys  |  |  |  |  |
| 1330 |     |     |     |     |     |     |     |     |     | 1335 |     |     |     |     | 1340 |  |  |  |  |
| Thr  | Cys | Thr | Thr | Cys | Cys | Cys | Ala | Thr | Cys | Cys  | Ala | Ala | Thr | Thr | Ala  |  |  |  |  |
| 1345 |     |     |     |     |     |     |     |     |     | 1350 |     |     |     |     | 1355 |  |  |  |  |
| Thr  | Gly | Thr | Gly | Ala | Ala | Gly | Cys | Thr | Gly | Ala  | Cys | Cys | Ala | Cys | Ala  |  |  |  |  |
| 1365 |     |     |     |     |     |     |     |     |     | 1370 |     |     |     |     | 1375 |  |  |  |  |
| Gly  | Ala | Cys | Ala | Thr | Gly | Gly | Ala | Cys | Cys | Cys  | Ala | Ala | Gly | Cys | Cys  |  |  |  |  |
| 1380 |     |     |     |     |     |     |     |     |     | 1385 |     |     |     |     | 1390 |  |  |  |  |
| Ala  | Gly | Cys | Ala | Ala | Thr | Gly | Ala |     |     |      |     |     |     |     |      |  |  |  |  |
| 1395 |     |     |     |     |     |     |     |     |     | 1400 |     |     |     |     |      |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Arg | Arg | Val | Ser | Lys | Arg | Arg | Met | Ala | Arg | Lys | Lys | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | His | Lys | Thr | Ser | Trp | Val | Gly | Phe | Ser | Ile | Asn | Thr | Lys | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gln | Leu | Ser | Gln | Leu | Ser | Arg | His | Pro | Gly | Pro | Leu | Gln | Lys | Lys | Gly |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Leu | Thr | Ile | Ser | Ala | Gln | Glu | Asn | Val | Lys | Val | Val | Tyr | Tyr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Tyr | Pro | Phe | Glu | Ser | Arg | Ser | His | Asp | Glu | Ile | Thr | Ile | Gln |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Pro | Gly | Asp | Ile | Val | Met | Val | Asp | Glu | Ser | Gln | Thr | Gly | Glu | Pro | Gly |



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Asn Tyr Val Lys Leu Thr Thr Asp Met Asp Pro Ser Gln Gln  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAATTCGCGG CCGCGTCGAC CAAGATCATT CCTGGGAGTG AAGTAAAACG GGAAGAACCA | 60  |
| GAAGCTTTGT ATGCAGCTGT AAATAAGAAA CCTACCTCGG CAGCCTATTC AGTTGGAGAA | 120 |
| GAATATATTG CACTTTATCC ATATTCAAGT GTGGAACCTG GAGATTTGAC TTTCACAGAA | 180 |
| GGTGAAGAAA TATTGGTGAC CCAGAAAGAT GGAGAGTGGT GGACAGGAAG TATTGGAGAT | 240 |
| AGAAGTGGAA TTTTTCATC AAACATATGTC AAACCAAAGG ATCAAGAGAG TTTTGGGAGT | 300 |
| GCTAGCAAGT CTGGAGCATC AAATAAAAAA CCTGAGATTG CTCAGGTAAC TTCAGCATAT | 360 |
| GTTGCTTCTG GTTCTGAACA ACTTAGCCTT GCACCAGGAC AGTTAATATT AATTCTAAAG | 420 |
| AAAAATACAA GTGGGTGGTG GCAAGGAGAG TTACAGGCCA GAGGAAAAAA GCGACAGAAA | 480 |
| GGATGGTTTC CTGCCAGTCA TGTTAACTT TTGGGTCCAA GCAGTGAAAG AGCCACACCT  | 540 |
| GCCTTTCATC CTGTATGTCA GGTGATTGCT ATGTATGACT ATGCAGCAA TAATGAAGAT  | 600 |
| GAGCTCAGTT TCTCCAAGGG ACAACTCATT AATGTTATGA ACAAAGATGA TCCTGATTGG | 660 |
| TGGCAAGGAG AGATCAACGG GGTGACTGGT CTCTTTCCTT CAACTACGT TAAGATGACG  | 720 |
| ACAGACTCAG ATCCAAGTCA ACAGTGA                                     | 747 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|                                                                 |           |
|-----------------------------------------------------------------|-----------|
| Glu Phe Ala Ala Ala Ser Thr Lys Ile Ile Pro Gly Ser Glu Val Lys | 1 5 10 15 |
| Arg Glu Glu Pro Glu Ala Leu Tyr Ala Ala Val Asn Lys Lys Pro Thr | 20 25 30  |
| Ser Ala Ala Tyr Ser Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr | 35 40 45  |
| Ser Ser Val Glu Pro Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile | 50 55 60  |

Leu Val Thr Gln Lys Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp  
 65 70 75 80  
 Arg Ser Gly Ile Phe Pro Ser Asn Tyr Val Lys Pro Lys Asp Gln Glu  
 85 90 95  
 Ser Phe Gly Ser Ala Ser Lys Ser Gly Ala Ser Asn Lys Lys Pro Glu  
 100 105 110  
 Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser Glu Gln Leu  
 115 120 125  
 Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser  
 130 135 140  
 Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys  
 145 150 155 160  
 Gly Trp Phe Pro Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu  
 165 170 175  
 Arg Ala Thr Pro Ala Phe His Pro Val Cys Gln Val Ile Ala Met Tyr  
 180 185 190  
 Asp Tyr Ala Ala Asn Asn Glu Asp Glu Leu Ser Phe Ser Lys Gly Gln  
 195 200 205  
 Leu Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu  
 210 215 220  
 Ile Asn Gly Val Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met Thr  
 225 230 235 240  
 Thr Asp Ser Asp Pro Ser Gln Gln  
 245

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Ser Gly Ser Arg Pro Pro Arg Trp Ser Pro Pro Pro Val Pro  
 1 5 10 15  
 Leu Pro Thr Ser Leu Asp Ser Arg  
 20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Gly Ser Gly Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr  
1 5 10 15  
Arg

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Glu Ser Gly Ser Arg Leu Gly Glu Phe Ser Lys Pro Pro Ile Pro  
1 5 10 15  
Gln Lys Pro Thr Trp Met Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Thr Val Pro Arg Trp Ile Glu Asp Ser Leu Arg Gly Gly Ala Ala  
1 5 10 15  
Arg Ala Gln Thr Arg Leu Ala Ser Ala Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Leu Pro Pro Leu Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Cys Trp Ser Glu Trp Asp Gly Asn Glu Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Cys Gly Gln Trp Ala Asp Asp Gly Tyr Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Cys Glu Xaa Trp Asp Gly Tyr Gly Ala Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Cys Trp Pro Phe Trp Asp Gly Ser Thr Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Cys Met Ile Trp Pro Asp Gly Glu Glu Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Glu Ser Xaa Trp Asp Gly Tyr Asp Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Cys Gln Gln Trp Lys Glu Asp Gly Trp Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: Other  
    (B) LOCATION: 4  
    (D) OTHER INFORMATION: Undefined  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:  
Cys Leu Tyr Xaa Trp Asp Gly Tyr Glu Cys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:54:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 10 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: unknown  
    (ii) MOLECULE TYPE: peptide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:  
Cys Met Gly Asp Asn Leu Gly Asp Asp Cys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:55:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 10 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: unknown  
    (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: Other  
    (B) LOCATION: 8  
    (D) OTHER INFORMATION: Undefined  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
Cys Met Gly Asp Ser Leu Gly Xaa Ser Cys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:56:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 10 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: unknown  
    (ii) MOLECULE TYPE: peptide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
Cys Met Asp Asp Asp Leu Gly Lys Gly Cys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:57:  
    (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Cys Met Gly Glu Asn Leu Gly Trp Ser Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Cys Leu Gly Glu Ser Leu Gly Trp Met Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gly Asp Gly Tyr Glu Glu Ile Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Asp Gly Tyr Asp Glu Pro Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Asp Gly Tyr Asp His Pro Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly Asp Gly Tyr Val Ile Pro Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Asp Gly Tyr Gln Asn Tyr Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Asp Gly Tyr Met Ala Met Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Asp Gly Gln Asn Tyr Ser Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Gly Ser Gly Ser Met Pro Pro Pro Val Pro Pro Arg Pro Pro Gly  
1 5 10 15  
Thr Leu Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Gly Ser Gly Asn Tyr Val Asn Ala Leu Pro Pro Gly Pro Pro Leu  
1 5 10 15  
Pro Ala Lys Asn Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Thr Val Ile Gln Asp Tyr Glu Pro Arg Leu Thr Asp Glu Ile Arg Ile

(2) INFORMATION FOR SEQ ID NO:69:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

(2) INFORMATION FOR SEQ ID NO:70:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

(2) INFORMATION FOR SEQ ID NO:71:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

- 55 -

Asn Lys Gly Glu Val Phe Arg Ala Val Asp Thr Leu Tyr Asn Gly Lys  
 20 25 30  
 Leu Gly Ser Ala Ile Arg Ile Gly Lys Asn His Lys Glu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Val Ala Ile Lys Ala Tyr Thr Ala Val Glu Gly Asp Glu Val Ser Leu  
 1 5 10 15  
 Leu Glu Gly Glu Ala Val Glu Val Ile His Lys Leu Leu Asp Gly Val  
 20 25 30  
 Ile Arg Lys Asp Asp Val Thr Gly Tyr  
 35 40

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Ala Ile Leu Pro Tyr Thr Lys Val Pro Asp Thr Asp Glu Ile Ser  
 1 5 10 15  
 Phe Leu Lys Gly Asp Met Phe Ile Val His Asn Glu Leu Glu Asp Met  
 20 25 30  
 Trp Val Thr Asn Leu Arg Thr  
 35

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Arg Ala Val Tyr Ala Tyr Glu Pro Gln Thr Pro Glu Glu Leu Ala Ile  
 1 5 10 15  
 Gln Glu Asp Asp Leu Leu Tyr Leu Leu Gln Lys Ser Asp Ile Asp Asp

20

25

30

Thr Val Lys Lys Arg Val Ile Gly Ser Asp  
 35 40

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Ala Lys Tyr Ser Tyr Gln Ala Gln Thr Ser Lys Glu Leu Ser Phe  
 1 5 10 15  
 Met Glu Gly Glu Phe Phe Tyr Val Ser Gly Asp Glu Lys Asp Lys Ala  
 20 25 30  
 Ser Asn Pro Ser Thr Gly Lys Glu  
 35 40

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala His Arg Val Leu Phe Gly Phe Val Pro Glu Thr Lys Glu Glu Leu  
 1 5 10 15  
 Gln Val Met Pro Gly Asn Ile Val Phe Val Leu Lys Lys Gly Asn Asp  
 20 25 30  
 Ala Thr Val Met Phe Asn Gly Gln Lys  
 35 40

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Arg Gly Ile Val Gln Tyr Asp Phe Met Ala Glu Ser Gln Asp Glu Leu  
 1 5 10 15  
 Thr Ile Lys Ser Gly Asp Lys Val Tyr Ile Leu Asp Asp Lys Lys Ser  
 20 25 30

Lys Asp Met Cys Gln Leu Val Asp Ser Gly Lys  
 35 40

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gln Ala Leu Phe Asp Pro Asp Pro Gln Glu Asp Gly Glu Leu Gly Phe  
 1 5 10 15  
 Arg Arg Gly Asp Phe Ile His Val Met Asp Asn Ser Asp Pro Asn Lys  
 20 25 30  
 Gly Ala Cys His Gly Gln  
 35

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gln Ala Leu Tyr Pro Phe Ser Ser Ser Asn Asp Glu Glu Leu Asn Phe  
 1 5 10 15  
 Glu Lys Gly Asp Val Met Asp Val Ile Glu Lys Pro Glu Asn Asp Pro  
 20 25 30  
 Glu Lys Cys Arg Lys Ile Asn Gly Met  
 35 40

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Val Ala Met Tyr Asp Phe Gln Ala Thr Glu Ala His Asp Leu Arg Leu  
 1 5 10 15  
 Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu Lys Asn Asp Leu His Arg  
 20 25 30  
 Ala Arg Asp Lys Tyr Gly Trp

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val Ala Leu Tyr Asp Tyr Asn Pro Met Asn Ala Asn Asp Leu Gln Leu  
 1 5 10 15  
 Arg Lys Gly Asp Glu Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Arg  
 20 25 30  
 Ala Arg Asp Lys Asn Gly Gln  
 35

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile  
 1 5 10 15  
 Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn Gly Glu  
 20 25 30  
 Glu Ala Gln Thr Lys Asn Gly Gln  
 35 40

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr Glu Thr Asp Leu Ser Phe  
 1 5 10 15  
 Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn Thr Glu Gly Asp Leu  
 20 25 30  
 Ala His Ser Leu Ser Thr Gly Gln  
 35 40

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe  
1 5 10 15  
Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly Asp Glu  
20 25 30  
Ala Arg Ser Leu Ser Ser Gly Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Ser Phe  
1 5 10 15  
His Lys Gly Glu Lys Phe Gln Ile Leu Asn Ser Ser Glu Gly Asp Glu  
20 25 30  
Ala Arg Ser Leu Thr Thr Gly Glu  
35 40

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
1 5 10 15  
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Glu  
20 25 30  
Ala Arg Ser Ile Ala Thr Gly Lys  
35 40



(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Gly Asp Asp Leu Thr Phe  
1 5 10 15  
Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Tyr Asp Glu  
20 25 30  
Ala Arg Ser Leu Ser Ser Gly His  
35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Ile Ser Glu Asp Leu Ser Phe  
1 5 10 15  
Lys Lys Gly Glu Arg Leu Gln Ile Ile Asn Thr Ala Asp Gly Asp Tyr  
20 25 30  
Ala Arg Ser Leu Ile Thr Asn Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe  
1 5 10 15  
Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Lys Ala  
20 25 30  
Arg Ser Leu Ala Thr Arg Lys  
35

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp Asp Leu Ser Phe  
 1 5 10 15  
 Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His Gly Glu Lys Ala  
 20 25 30  
 Lys Ser Leu Leu Thr Lys Lys  
 35

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Leu Pro Asp Tyr Ala Ala Val Asn Asp Arg Asp Leu Gln Val  
 1 5 10 15  
 Leu Lys Gly Glu Lys Leu Gln Val Leu Arg Ser Thr Gly Asp Leu Ala  
 20 25 30  
 Arg Ser Leu Val Thr Gly Arg  
 35

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu Gly Phe  
 1 5 10 15  
 Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu Lys Ala  
 20 25 30  
 Gln Ser Leu Thr Thr Gly Gln  
 35

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Ala Lys Phe Asp Tyr Val Ala Gln Gln Glu Gln Glu Leu Asp Ile  
 1 5 10 15  
 Lys Lys Asn Glu Arg Leu Trp Leu Leu Asp Asp Ser Lys Ser Trp Val  
 20 25 30  
 Arg Asn Ser Met Asn Lys  
 35

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Arg Ala Ile Tyr Asp Tyr Glu Gln Val Gln Asn Ala Asp Glu Glu Leu  
 1 5 10 15  
 Thr Phe His Glu Asn Asp Val Phe Asp Val Phe Asp Asp Lys Asp Ala  
 20 25 30  
 Asp Leu Val Lys Ser Thr Val Ser Asn Glu  
 35 40

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe  
 1 5 10 15  
 Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly Arg  
 20 25 30  
 Gly Arg Cys His Gly His  
 35

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Thr Ala Glu Tyr Asp Tyr Asp Ala Ala Glu Asp Asn Glu Leu Thr Phe  
 1 5 10 15  
 Val Glu Asn Asp Lys Ile Ile Asn Ile Glu Phe Val Asp Asp Asp Leu  
 20 25 30  
 Gly Glu Leu Glu Lys Asp Gly Ser  
 35 40

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Tyr Val Lys Phe Asn Tyr Asn Ala Glu Arg Glu Asp Glu Leu Ser Leu  
 1 5 10 15  
 Ile Lys Gly Thr Lys Val Ile Val Met Glu Lys Cys Ser Asp Gly Arg  
 20 25 30  
 Gly Ser Tyr Asn Gly Gln  
 35

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Ala Arg Tyr Asp Phe Cys Ala Arg Asp Arg Ser Glu Leu Ser Leu  
 1 5 10 15  
 Lys Glu Gly Asp Ile Ile Lys Ile Leu Asn Lys Lys Gly Gln Gln Trp  
 20 25 30  
 Arg Gly Glu Ile Tyr Gly Arg  
 35

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ile Ala Lys Tyr Asp Phe Lys Ala Thr Ala Asp Asp Glu Leu Ser Phe  
1 5 10 15  
Lys Arg Gly Asp Ile Leu Lys Val Leu Asn Glu Glu Cys Asp Gln Tyr  
20 25 30  
Lys Ala Glu Leu Asn Gly Lys  
35

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Lys Ala Leu Tyr Asp Tyr Lys Ala Lys Arg Ser Asp Glu Leu Ser Phe  
1 5 10 15  
Cys Arg Gly Ala Leu Ile His Asn Val Ser Lys Glu Pro Gly Trp Lys  
20 25 30  
Gly Asp Tyr Gly Thr Arg Ile  
35

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Lys Ala Leu Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe  
1 5 10 15  
Ile Lys Ser Ala Ile Ile Gln Asn Val Glu Lys Gln Glu Gly Trp Arg  
20 25 30  
Gly Asp Tyr Gly Gly Lys Lys  
35

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Lys Ala Leu Tyr Asp Tyr Asp Ala Gln Thr Gly Asp Glu Leu Thr Phe  
1 5 10 15

Lys Glu Gly Asp Thr Ile Ile Val His Gln Lys Asp Pro Ala Trp Glu  
20 25 30

Gly Glu Leu Asn Gly Lys  
35

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Arg Ala Leu Tyr Asp Phe Ala Ala Glu Asn Pro Asp Glu Leu Thr Phe  
1 5 10 15

Asn Glu Gly Ala Val Val Thr Val Ile Asn Lys Ser Asn Pro Trp Glu  
20 25 30

Gly Glu Leu Asn Gly Gln  
35

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Lys Ala Leu Tyr Asp Tyr Asp Ala Ser Ser Thr Asp Glu Leu Ser Phe  
1 5 10 15

Lys Glu Gly Asp Ile Ile Phe Ile Val Gln Lys Asp Asn Gly Thr Gln  
20 25 30

Gly Glu Leu Lys Ser Gly Gln  
35

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu Ala Leu Phe Ser Tyr Glu Ala Thr Gln Pro Glu Asp Leu Glu Phe  
1 5 10 15  
Gln Glu Gly Asp Ile Ile Leu Val Leu Ser Lys Val Asn Glu Leu Glu  
20 25 30  
Gly Glu Cys Lys Gly Lys  
35

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Arg Ala Ile Ala Asp Tyr Glu Lys Thr Ser Gly Ser Glu Met Ala Leu  
1 5 10 15  
Ser Thr Gly Asp Val Val Glu Val Val Glu Lys Ser Glu Ser Gly Phe  
20 25 30  
Cys Gln Met Lys Ala Lys  
35

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ala Leu Val Asp Phe Gln Ala Arg Ser Pro Arg Glu Val Thr Met  
1 5 10 15  
Lys Lys Gly Asp Val Leu Thr Leu Leu Ser Ser Ile Asn Lys Asp Lys  
20 25 30  
Val Glu Ala Ala Asp His  
35

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Tyr Ala Ile Val Leu Tyr Asp Phe Lys Ala Glu Lys Ala Asp Glu Leu  
1 5 10 15  
Thr Thr Tyr Val Gly Glu Asn Leu Phe Ile Cys Ala His His Asn Cys  
20 25 30  
Glu Ile Ala Lys Pro Ile Gly Arg Leu Gly Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Ala Ala Tyr Asp Phe Asn Tyr Pro Ile Lys Lys Asp Ser Ser Ser  
1 5 10 15  
Gln Leu Leu Ser Val Gln Gln Gly Glu Thr Ile Tyr Ile Leu Asn Lys  
20 25 30  
Asn Ser Ser Gly Asp Gly Leu Val Ile Asp Asp  
35 40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Arg Phe Gln Thr Thr Ala Ile Ser Asp Tyr Glu Asn Ser Ser Asn  
1 5 10 15  
Pro Ser Phe Leu Lys Phe Ser Ala Gly Asp Thr Ile Ile Val Ile Glu  
20 25 30  
Val Leu Glu Asp Cys Asp Gly  
35

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:



Arg Ala Leu Val Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp Leu  
 1 5 10 15  
 His Leu Gly Asp Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu  
 20 25 30  
 Gly Phe Ser Asp Gly Gln Glu Ala Arg Pro Glu Glu Ile Leu Asn Gly  
 35 40 45  
 Tyr Asn Glu Thr Thr Gly Glu  
 50 55

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asn Lys Gly Thr Val Tyr Ala Leu Trp Asp Tyr Glu Ala Gln Asn Ser  
 1 5 10 15  
 Asp Glu Leu Ser Phe His Glu Gly Asp Ala Ile Thr Ile Leu Arg Arg  
 20 25 30  
 Lys Asp Glu Asn Glu Thr Glu Trp Trp Trp Ala Arg Leu Gly Asp Arg  
 35 40 45  
 Glu Gly Tyr Val Pro Lys Asn Leu Leu Gly Leu Tyr  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro  
 1 5 10 15  
 Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met  
 20 25 30  
 Ser Asp Thr Ser Trp Trp Lys Gly Thr Cys Lys Gly Arg Thr Gly Leu  
 35 40 45  
 Ile Pro Ser Asn Tyr Val Ala Glu Gln  
 50 55

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

His Trp Thr Pro Tyr Arg Ala Met Tyr Gln Tyr Arg Pro Gln Asn Glu  
1 5 10 15  
Asp Glu Leu Glu Leu Arg Glu Gly Asp Arg Val Asp Val Met Gln Gln  
20 25 30  
Cys Asp Asp Gly Trp Phe Val Gly Val Ser Arg Arg Thr Gln Lys Phe  
35 40 45  
Gly Thr Phe Pro Gly Asn Tyr Val Ala Pro Val  
50 55

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Gln Pro Ser Cys Lys Ala Leu Tyr Asp Phe Glu Pro Glu Asn Asp  
1 5 10 15  
Gly Glu Leu Gly Phe Arg Glu Gly Asp Leu Ile Thr Leu Thr Asn Gln  
20 25 30  
Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser Gly Phe  
35 40 45  
Phe Pro Leu Ser Tyr Val Gln Val Leu  
50 55

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Gly Ile Thr Ala Ile Ala Leu Tyr Asp Tyr Gln Ala Ala Gly Asp  
1 5 10 15  
Asp Glu Ile Ser Phe Asp Pro Asp Asp Ile Ile Thr Asn Ile Glu Met  
20 25 30  
Ile Asp Asp Gly Trp Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu  
35 40 45

Phe Pro Ala Asn Tyr Val Glu Leu Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gly Gly Lys Arg Tyr Arg Ala Val Tyr Asp Tyr Ser Ala Ala Asp Glu  
1 5 10 15  
Asp Glu Val Ser Phe Gln Asp Gly Asp Thr Ile Val Asn Val Gln Gln  
20 25 30  
Ile Asp Asp Gly Trp Met Tyr Gly Thr Val Glu Arg Thr Gly Asp Thr  
35 40 45  
Gly Met Leu Pro Ala Asn Tyr Val Glu Ala Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp  
1 5 10 15  
Thr Glu Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val  
20 25 30  
Ile Asp Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly  
35 40 45  
Met Phe Pro Ala Asn Tyr Val Glu Leu Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Gln Pro Cys Cys Arg Ala Leu Tyr Asp Leu Glu Pro Glu Asn Glu

|                                                                 |                         |                             |    |
|-----------------------------------------------------------------|-------------------------|-----------------------------|----|
| 1                                                               | 5                       | 10                          | 15 |
| Gly Glu Leu                                                     | Ala Phe Lys Glu Gly Asp | Ile Ile Thr Leu Thr Asn Gln |    |
|                                                                 | 20                      | 25                          | 30 |
| Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser Gly Phe |                         |                             |    |
|                                                                 | 35                      | 40                          | 45 |
| Phe Pro Ile Asn Tyr Val Glu Ile Leu                             |                         |                             |    |
|                                                                 | 50                      | 55                          |    |

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Phe Met Phe Lys Val Gln Ala Gln His Asp Tyr Thr Ala Thr Asp Thr |          |
| 1                                                               | 5 10 15  |
| Asp Glu Leu Gln Leu Lys Ala Gly Asp Val Val Leu Val Ile Pro Phe |          |
|                                                                 | 20 25 30 |
| Gln Asn Pro Glu Glu Gln Asp Glu Gly Trp Leu Met Gly Val Lys Glu |          |
|                                                                 | 35 40 45 |
| Ser Asp Trp Asn Gln His Lys Glu Leu Glu Lys Cys Arg Gly Val Phe |          |
|                                                                 | 50 55 60 |
| Pro Glu Asn Phe Thr Glu Arg Val                                 |          |
| 65                                                              | 70       |

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Phe Met Lys Lys Val Gln Ala Gln His Asp Tyr Thr Ala Thr Asp Thr |          |
| 1                                                               | 5 10 15  |
| Asp Glu Leu Gln Leu Lys Ala Gly Asp Val Val Leu Val Ile Pro Phe |          |
|                                                                 | 20 25 30 |
| Gln Asn Pro Glu Glu Gln Asp Glu Gly Trp Leu Met Gly Val Lys Glu |          |
|                                                                 | 35 40 45 |
| Ser Asp Trp Asn Gln His Lys Glu Leu Glu Lys Cys Arg Gly Val Phe |          |
|                                                                 | 50 55 60 |
| Pro Glu Asn Phe Thr Glu Arg Val                                 |          |
| 65                                                              | 70       |

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Gly Ile Ser Ala Ile Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser  
1 5 10 15  
Asp Glu Leu Ser Phe Asp Pro Asp Asp Ile Ile Thr Asp Ile Glu Met  
20 25 30  
Val Asp Glu Gly Trp Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu  
35 40 45  
Phe Pro Ala Asn Tyr Val Lys Leu Leu  
50 55

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Glu Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu  
1 5 10 15  
Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys  
20 25 30  
Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly  
35 40 45  
Met Ile Pro Val Pro Tyr Val Glu Lys Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys Thr Ala Leu  
1 5 10 15  
Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile Asn Val Ser  
20 25 30

Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His Phe Pro Phe  
 35 40 45  
 Thr His Val Arg Leu Leu  
 50

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu Met Arg Pro Ala Arg Ala Lys Phe Asp Phe Lys Ala Gln Thr Leu  
 1 5 10 15  
 Lys Glu Leu Pro Leu Gln Lys Gly Asp Val Val Tyr Ile Tyr Arg Gln  
 20 25 30  
 Ile Asp Gln Asn Trp Tyr Glu Gly Glu His His Gly Arg Val Gly Ile  
 35 40 45  
 Phe Pro Arg Thr Tyr Ile Glu Leu Leu  
 50 55

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Glu Tyr Gly Glu Ala Ile Ala Lys Phe Asn Phe Asn Gly Asp Thr Gln  
 1 5 10 15  
 Val Glu Met Ser Phe Arg Lys Gly Glu Arg Ile Thr Leu Leu Arg Gln  
 20 25 30  
 Val Asp Glu Asn Trp Tyr Glu Gly Arg Ile Pro Gly Thr Ser Arg Gln  
 35 40 45  
 Gly Ile Phe Pro Ile Thr Tyr Val Asp Val Leu  
 50 55

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Asp Leu Cys Ser Tyr Gln Ala Leu Tyr Ser Tyr Val Pro Gln Asn Asp  
1 5 10 15  
Asp Glu Leu Glu Leu Arg Asp Gly Asp Ile Val Asp Val Met Glu Lys  
20 25 30  
Cys Asp Asp Gly Trp Phe Val Gly Thr Ser Arg Arg Thr Arg Gln Phe  
35 40 45  
Gly Thr Phe Pro Gly Asn Tyr Val Lys Pro Leu  
50 55

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Gln Pro Cys Cys Arg Gly Leu Tyr Asp Phe Glu Pro Glu Asn Glu  
1 5 10 15  
Gly Glu Leu Gly Phe Lys Glu Gly Asp Ile Ile Thr Leu Thr Asn Gln  
20 25 30  
Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu Arg Gly Glu Ser Gly Phe  
35 40 45  
Phe Pro Ile Asn Tyr Val Glu Val Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Thr Glu Val Arg Val Arg Ala Leu Tyr Asp Tyr Glu Gly Gln Glu His  
1 5 10 15  
Asp Glu Leu Ser Phe Lys Ala Gly Asp Glu Leu Thr Lys Met Glu Asp  
20 25 30  
Glu Asp Glu Gln Gly Trp Cys Lys Gly Arg Leu Asp Asn Gly Gln Val  
35 40 45  
Gln Leu Tyr Pro Ala Asn Tyr Val Glu Ala Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:130:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Val | Arg | Val | Arg | Ala | Leu | Tyr | Asp | Tyr | Asp | Gly | Gln | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Leu | Ser | Phe | Lys | Ala | Gly | Asp | Glu | Leu | Thr | Lys | Leu | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Asp | Glu | Gln | Gly | Trp | Cys | Arg | Gly | Arg | Leu | Asp | Ser | Gly | Gln | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Tyr | Pro | Ala | Asn | Tyr | Val | Glu | Ala | Ile |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gly | Asp | Ile | Val | Val | Ala | Leu | Tyr | Pro | Tyr | Asp | Gly | Ile | His | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asp | Leu | Ser | Phe | Lys | Lys | Gly | Glu | Lys | Met | Lys | Val | Leu | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gly | Glu | Trp | Trp | Lys | Ala | Lys | Ser | Leu | Leu | Thr | Lys | Lys | Glu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ile | Pro | Ser | Asn | Tyr | Val | Ala | Lys | Leu |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

|          |     |     |           |          |     |     |     |           |           |     |     |     |           |           |     |
|----------|-----|-----|-----------|----------|-----|-----|-----|-----------|-----------|-----|-----|-----|-----------|-----------|-----|
| Gly<br>1 | Val | Thr | Leu       | Phe<br>5 | Val | Ala | Leu | Tyr       | Asp<br>10 | Tyr | Glu | Ala | Arg       | Thr<br>15 | Glu |
| Asp      | Asp | Leu | Ser<br>20 | Phe      | His | Lys | Gly | Glu<br>25 | Lys       | Phe | Gln | Ile | Leu<br>30 | Asn       | Ser |
| Ser      | Glu | Gly | Asp       | Trp      | Trp | Glu | Ala | Arg       | Ser       | Leu | Thr | Thr | Gly       | Glu       | Thr |



Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val  
50 55

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg Ser His  
1 5 10 15  
Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp Glu Ser  
20 25 30  
Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly Lys Thr  
35 40 45  
Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Glu Gly Leu Gln Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp  
1 5 10 15  
Asn His Leu Asn Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu Gln  
20 25 30  
Gln Asp Met Trp Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp Phe  
35 40 45  
Pro Lys Ser Tyr Val Lys Leu Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Glu Glu Ile Ala Gln Val Ile Ala Ser Tyr Thr Ala Thr Gly Pro  
 1 5 10 15  
 Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys  
 20 25 30  
 Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys  
 35 40 45  
 Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu Leu  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Thr Ala Gln Asn Asp  
 1 5 10 15  
 Asp Glu Leu Ala Phe Asn Lys Gly Gln Ile Ile Asn Val Leu Asn Lys  
 20 25 30  
 Glu Asp Pro Asp Trp Trp Lys Gly Glu Val Asn Gly Gln Val Gly Leu  
 35 40 45  
 Phe Pro Ser Asn Tyr Val Lys Leu Thr  
 50 55

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr Ser Ser Val Glu Pro  
 1 5 10 15  
 Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys  
 20 25 30  
 Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp Arg Ser Gly Ile Phe  
 35 40 45  
 Pro Ser Asn Tyr Val Lys Pro Lys  
 50 55

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser
1 5 10 15
Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys
20 25 30
Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys
35 40 45
Arg Gln Lys Gly Trp Phe Pro Ala Ser Tyr Val Lys Leu Leu
50 55 60

```

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

Pro Val Cys Gln Val Ile Gly Met Tyr Asp Tyr Ala Ala Asn Asn Glu
1 5 10 15
Asp Glu Leu Ser Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys
20 25 30
Asp Asp Pro Asp Trp Trp Gln Gly Glu Ile Asn Gly Val Thr Gly Leu
35 40 45
Phe Pro Ser Asn Tyr Val Leu Glu Glu
50 55

```

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr Glu
1 5 10 15
Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn
20 25 30
Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln Thr
35 40 45

```

Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Gly Pro Gly Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

His Gly Pro Thr Pro Pro Pro Pro Tyr Thr Val Gly Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Tyr Val Gln Pro Pro Pro Pro Pro Tyr Pro Gly Pro Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Pro Gly Tyr Pro Tyr Pro Pro Pro Pro Glu Phe Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Pro Gly Thr Pro Ala Pro Pro Tyr Thr Val Gly Pro Gly Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Thr Pro Pro Ala Pro Tyr Thr Val Gly Pro Gly Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Asp Ser Gly Val Arg Pro Leu Pro Pro Leu Pro Asp Pro Gly Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Val Arg Pro Leu Pro Pro Leu Pro Glu Glu Leu Pro Arg Pro Arg Arg  
1 5 10 15  
Pro Pro Pro Glu Asp  
20

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Pro Pro Pro Ala Leu Pro Pro Pro Pro Arg Pro Val Ala Asp Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala Pro Ala Pro Pro Pro Gly Pro Pro Arg Pro Ala Ala Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Gly Gly Gly Phe Pro Pro Leu Pro Pro Pro Pro Tyr Leu Pro Pro Leu  
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ser Ile Ser Pro Arg Pro Arg Pro Pro Gly Arg Pro Val Ser Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Pro Pro Pro Glu His Ile Pro Pro Pro Pro Arg Pro Lys Arg Ile Leu  
1                      5                      10                      15  
Glu

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Lys Glu Gly Glu Arg Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Ser Arg Leu Lys Pro Ala Pro Pro Pro Pro Pro Ala Ala Ser Ala Gly  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Gln Ala Ser Leu Pro Pro Val Pro Pro Arg Asp Leu Leu Leu Pro  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro Asp  
1                      5                      10                      15  
Arg Pro Tyr Ser  
                    20

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Ser Asp Gln Gly Arg Asn Leu Pro Gly Thr Pro Val Pro Ala Ser  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg His Ser Arg Arg Gln Leu Pro Pro Val Pro Pro Lys Pro Arg Pro  
1                      5                      10                      15  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Glu Lys Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met



Thr Tyr

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gln | Pro | His | Arg | Val | Leu | Pro | Thr | Ser | Pro | Ser | Asp | Ile | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asp | Phe | Gln | Pro | Pro | Tyr | Phe | Pro | Pro | Pro | Tyr | Gln | Pro | Ile | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |

Pro Gln Ser

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ala | Ala | Pro | Pro | Pro | Pro | Pro | Arg | Arg | Ala | Thr | Pro | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Lys Lys Gly Val Met Thr Ala Pro Pro Pro Pro Pro Pro Val  
1 5 10 15  
Tyr Glu Pro Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Glu Ala Phe Gln Pro Gln Glu Pro Asp Phe Pro Pro Pro Pro Pro Asp  
1 5 10 15  
Leu Glu

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Asp Glu Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val Pro  
1 5 10 15  
Pro Pro Arg Pro Pro Pro Pro Glu  
20

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Pro Gln Arg Arg Ala Pro Ala Val Pro Pro Ala Arg Pro Gly Ser Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Leu Gly Gly Ala Pro Pro Val Pro Ser Arg Pro Gly Ala Ser Pro Asp  
 1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Pro Pro Pro Pro Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg  
 1 5 10 15

Gly Asn His

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Ala Ala Glu Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Asp  
 1 5 10 15

Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Asp Glu Glu Val Asn Ile Pro Pro His Thr Pro Val Arg Thr Val

1

5

10

15

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ser Ala Glu Gly Asn Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg  
1                      5                      10                      15  
Phe Asp

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Ala Trp Met Trp Gly Ser Pro Pro Glu Glu Glu Gly Trp Phe  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala Glu Trp Leu Glu Gly Pro Pro Trp Tyr Asp Arg Lys Glu Gly Phe  
1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Gly Leu Glu Gly Trp Tyr Trp Glu Arg Gly Trp Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Trp Gly Leu Asp Gly Trp Leu Val Asp Gly Trp Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Leu Lys Arg Pro Leu Pro Pro Leu Pro Val Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Ser Arg Ser Leu Ser Glu Val Ser Pro Lys Pro Pro Ile Arg Ser Val  
1 5 10 15

Ser Leu Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ser Arg Pro Pro Arg Trp Ser Pro Pro Pro Val Pro Leu Pro Thr Ser  
1 5 10 15

Leu Asp Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Ser Arg Leu Gly Glu Phe Ser Lys Pro Pro Ile Pro Gln Lys Pro Thr  
1 5 10 15

Trp Met Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Ser Phe Ala Ala Pro Ala Arg Pro Pro Val Pro Pro Arg Lys Ser Arg  
1 5 10 15  
Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Ser Tyr Asp Ala Ser Ser Ala Pro Gln Arg Pro Pro Leu Pro Val Arg  
1 5 10 15  
Lys Ser Arg Pro Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ser Pro Pro Pro Val Pro Pro Arg Pro Pro Ala Thr Leu Gly Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Ser Val Pro Ala Pro Pro Pro Leu Pro Pro Lys Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ser Phe Ser Phe Pro Pro Leu Pro Pro Ala Pro Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Ser Val Pro Leu Pro Pro Leu Arg Thr Val Ser Leu Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1710 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACTCTCTAC ACTTGCACCG GCATCAAGGA CGAAAAGAAC GCGCTAGATA TGA        | 60  |
| GCTGCTCAAG ACAATGAACT TACTTTCAAA GCTGGAGAAA TTATGACAGT TCTTGATGAC | 120 |
| AGTGATCCTA ACTGGTGGAA AGGTGAAACC CATCAAGGCA TAGGGTTATT TCCTTCTAAT | 180 |
| TTTGTGACTG CAGATCTCAC TGCTGAACCA GAAATGATTA AAACAGAGAA GAAGACGGTA | 240 |
| CAATTTAGTG ATGATGTTCA GGTAGAGACA ATAGAACCAG AGCCGGAACC AGCCTTTATT | 300 |
| GATGAAGATA AAATGGACCA GTTGCTACAG ATGCTGCAAA GTACAGACCC CAGTGATGAT | 360 |
| CAGCCAGACC TACCAGAGCT GCTTCATCTT GAAGCAATGT GTCACCAGAT GGGACCTCTC | 420 |
| ATTGATGAAA AGCTGGAAGA TATTGATAGA AAACATTGAG AACTCTCAGA ACTTAATGTG | 480 |
| AAAGTGATGG AGGCCCTTTC CTTATATACC AAGTTAATGA ACGAAGATCC GATGTATTCC | 540 |
| ATGTATGCAA AGTTACAGAA TCAGCCATAT TATATGCAGT CATCTGGTGT TTCTGGTTCT | 600 |
| CAGGTGTATG CAGGGCCTCC TCCAAGTGGT GCCTACCTGG TTGCAGGGAA CGCGCAGATG | 660 |
| AGCCACCTCC AGAGCTACAG TCTTCCCCCG GAGCAGCTGT CTTCTCTCAG CCAGGCAGTG | 720 |
| GTCCCACCAT CCGCAAACCC AGCCCTTCCT AGTCAGCAGA CTCAGGCCGC TTACCCAAAC | 780 |
| CGCTCCCCAG GGGACCTCAT GAAGCCCGGT GATTCTGAAT GCCGTGGATC TGCCGAGGAT | 840 |
| TCCCAGATGC GTATTTCTCC TCCGTACTTC CCCACAGGAC AGCAGGCTTG AATAGCTGAT | 900 |
| TGCCTATGCA GGACAACAGG CTTGAATAGC TGA                              | 960 |



GTTTTTTGGG CATCAAACTT GACAGATCCA AGATTATTAC TTTGATCTTC CCCACACCCC 1020  
 TCCCACCCCC GAGTCTACTA TGGTCCCATC ATAGTATTCT GAAAATCAGT GAATGGCCAC 1080  
 TCTACCAGTT ATTTCTACCA GTTTTTAGGT TCTAAACCTC AGGCATTCTG GACTCTTCTG 1140  
 TTCATTATCA TATTTTGAAG GCATTATCTT CAAAATCTAT CTAGACTCTG ACCCTTTCTC 1200  
 CCATCTCCAC CATTACTGCC GTGGCTCTTC TGCTGGTCGG CTCTCTCCTG GTGGATCCGT 1260  
 AATAACCTGC AGTCAGCTAT CCTGGTCCAG AAGGGAACCC CGTTAAACCC TGTGGAATC 1320  
 TTATCACGCT TCTGCTCCAG AACGAACCCA GTCTGTCTGT CTCACTCAGA GTGTAAGCTA 1380  
 CAGTCCTTAT TGTGGCCATC AGGTGCTGTG TGTCTCCAG CCCCCTCCCC ACCACCGCAG 1440  
 TCCTGCCGGT GATCTTAGCT GCTCTCCCCT CGGAACCCCC TCGGGCCCCC TCTGCCGCAA 1500  
 CANTCGTGGC CTGCTGTTCC TTGAACATGC TTGGTGT TTTT CTCTCCTCAA AGGCTTCTTT 1560  
 CTGTTTACCT GAAATGTACT TGCCTAGGGA AATCTTATCC TGGCTCACTC CGCTTACTTT 1620  
 TTTCCACATC TTTGCTTAAA GTTATTGCCC TTATTGGAGA AGGCACCCCT ACCATAAACT 1680  
 AGAAATCCCT TGCCCCCAAG CTGTTCTTTT 1710

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

His Ser Leu His Leu His Arg His Gln Gly Arg Lys Glu Arg Ala Arg  
 1 5 10 15  
 Tyr Asp Leu Glu Ala Ala Gln Asp Asn Glu Leu Thr Phe Lys Ala Gly  
 20 25 30  
 Glu Ile Met Thr Val Leu Asp Asp Ser Asp Pro Asn Trp Trp Lys Gly  
 35 40 45  
 Glu Thr His Gln Gly Ile Gly Leu Phe Pro Ser Asn Phe Val Thr Ala  
 50 55 60  
 Asp Leu Thr Ala Glu Pro Glu Met Ile Lys Thr Glu Lys Lys Thr Val  
 65 70 75 80  
 Gln Phe Ser Asp Asp Val Gln Val Glu Thr Ile Glu Pro Glu Pro Glu  
 85 90 95  
 Pro Ala Phe Ile Asp Glu Asp Lys Met Asp Gln Leu Leu Gln Met Leu  
 100 105 110  
 Gln Ser Thr Asp Pro Ser Asp Asp Gln Pro Asp Leu Pro Glu Leu Leu  
 115 120 125  
 His Leu Glu Ala Met Cys His Gln Met Gly Pro Leu Ile Asp Glu Lys  
 130 135 140  
 Leu Glu Asp Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val

|                                                                 |     |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
| 145                                                             |     | 150 |     | 155 |     | 160 |
| Lys Val Met Glu Ala Leu Ser Leu Tyr Thr Lys Leu Met Asn Glu Asp | 165 |     | 170 |     | 175 |     |
| Pro Met Tyr Ser Met Tyr Ala Lys Leu Gln Asn Gln Pro Tyr Tyr Met | 180 |     | 185 |     | 190 |     |
| Gln Ser Ser Gly Val Ser Gly Ser Gln Val Tyr Ala Gly Pro Pro Pro | 195 |     | 200 |     | 205 |     |
| Ser Gly Ala Tyr Leu Val Ala Gly Asn Ala Gln Met Ser His Leu Gln | 210 |     | 215 |     | 220 |     |
| Ser Tyr Ser Leu Pro Pro Glu Gln Leu Ser Ser Leu Ser Gln Ala Val | 225 |     | 230 |     | 235 | 240 |
| Val Pro Pro Ser Ala Asn Pro Ala Leu Pro Ser Gln Gln Thr Gln Ala | 245 |     | 250 |     | 255 |     |
| Ala Tyr Pro Asn Arg Ser Pro Gly Asp Leu Met Lys Pro Gly Asp Ser | 260 |     | 265 |     | 270 |     |
| Glu Cys Arg Gly Ser Ala Glu Asp Ser Gln Met Arg Ile Ser Pro Pro | 275 |     | 280 |     | 285 |     |
| Tyr Phe Pro Thr Gly Gln Gln Ala                                 | 290 |     | 295 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAATTCGCGG CCGCGTCGAC CAAGGAGAGT GGCCGCTTCC AGGACGTGGG ACCCCAGGCC | 60  |
| CCAGTGGGCT CTGTGTACCA GAAGACCAAT GCCGTGTCAG AGATTAAAG GGTGTTAG    | 120 |
| ACAGCTTCTG GGCCAAAGCA GAGAAGGAGG AGGAGAACCG TCGGCTGGAG GAAAAGCGGT | 180 |
| GGGCCGAGGA GGCACAGCGG CAGCTGGAGC AGGAGCGCCG GGAGCGTGAG CTGCGTGAGG | 240 |
| CTGCACGCCG GGAGCAGCGC TATCAGGAGC AGGGTGGCGA GGCCAGCCCC CAGAGCAGGA | 300 |
| CGTGGGAGCA GCAGCAAGAA GTGGTTTCAA GGAACCGAAA TGAGCAGGAG TCTGCCGTGC | 360 |
| ACCCGAGGGA GATTTTCAAG CAGAAGGAGA GGGCCATGTC CACCACCTCC ATCTCCAGTC | 420 |
| CTCAGCCTGG CAAGCTGAGG AGCCCCTTCC TGCAGAAGCA GCTCACCCAA CCAGAGACCC | 480 |
| ACTTTGGCAG AGAGCCAGCT GCTGCCATCT CAAGGCCAG GGCAGATCTC CCTGCTGAGG  | 540 |
| AGCCGGCGCC CAGCACTCCT CCATGTCTGG TGCAGGCAGA AGAGGAGGCT GTGTATCAGG | 600 |
| AACCTCCAGA GCAGGAGACC TTCTACGAGC AGCCCCACT GGTGCAGCAG CAAGGTGCTG  | 660 |
| GCTCTGAGCA CATTGACCAC CACATTCAGG GCCAGGGGCT CAGTGGGCAA GGGCTCTGTG | 720 |
| CCCGTGCCCT GTACGACTAC CAGGCAGCCC ACGACACAGA GATCTCCTTT GACCCCGAGA | 780 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ACCTCATCAC GGGCATCGAG GTGATCGACG AAGGCTGGTG GCGTGGCTAT GGGCCGGATG | 840  |
| GCCATTTTGG CATGTTCCCT GCCAATTACG TGGAGCTCAT TGATGAGGCT GAGGGCACAT | 900  |
| CTTGCCCTTC CCCTCTCAGA CATGGCTTCC TTATTGCTGG AAGAGGAGGC CTGGGAGTTG | 960  |
| ACATTCAGCA CTCTTCCAGG AATAGGACCC CCAGTGAGGA TGAGGCCTCA GGGCTCCCTC | 1020 |
| CGGCTTGGCA GACTCAGCCT GTCACCCCAA ATGCAGCAAT GGCCTGGTGA TTCCCACACA | 1080 |
| TCCTTCTGTC ATCCCCGAC CCTCCCAGAC AGCTTGGCTC TTGCCCCTGA CAGGATACTG  | 1140 |
| AGCCAAGCCC TGCCTGTGGC CAAGCCCTGA GTGGCCACTG CCAAGCTGCG GGGAAGGGTC | 1200 |
| CTGAGCAGGG GCATCTGGGA GGCTCTGGCT GCCTTCTGCA TTTATTGCG TTTTTCTTT   | 1260 |
| TTCTCTTGCT TCTAAGGGGT GGTGGCCACC ACTGTTTAGA ATGACCCTTG GGAACAGTGA | 1320 |
| ACGTAGAGAA TTGTTTTTAG CAGAGTTTGT GACCAAAGTC AGAGTGGATC ATGGTGGTTT | 1380 |
| GGCAGCAGGG AATTTGTCTT GTTGGAGCCT GCTCTGTGCT CCCCCTCCA TTTCTCTGTC  | 1440 |
| CCTCTGCCTG GGCTATGGGA AGTGGGGATG CAGATGGCCA AGCTCCCACC CTGGGTATTC | 1500 |
| AAAAACGGCA GACACAACAT GTTCTCCAC GCGGCTCACT CGATGCCTGC AGGCCCCAGT  | 1560 |
| GTGTGCCTCA ACTGATTCTG ACTTCAGGAA AAGTAACACA GAGTGGCCTT GGCCTGTTGT | 1620 |
| CTTCCCCTAT TTTCTGTCCC AGCTCATCCG TGGTCGAAGC GCCCGCGAAT TCCAGCTGAG | 1680 |
| CGGCCGC                                                           | 1687 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Ile | Arg | Gly | Arg | Val | Asp | Gln | Gly | Glu | Trp | Pro | Leu | Pro | Gly | Arg | Gly | 1   | 5   | 10  | 15 |
| Thr | Pro | Gly | Pro | Ser | Gly | Leu | Cys | Val | Pro | Glu | Asp | Gln | Cys | Arg | Val | 20  | 25  | 30  |    |
| Arg | Asp | Leu | Lys | Gly | Trp | Leu | Asp | Ser | Phe | Trp | Ala | Lys | Ala | Glu | Lys | 35  | 40  | 45  |    |
| Glu | Glu | Glu | Asn | Arg | Arg | Leu | Glu | Glu | Lys | Arg | Trp | Ala | Glu | Glu | Ala | 50  | 55  | 60  |    |
| Gln | Arg | Gln | Leu | Glu | Gln | Glu | Arg | Arg | Glu | Arg | Glu | Leu | Arg | Glu | Ala | 65  | 70  | 75  | 80 |
| Ala | Arg | Arg | Glu | Gln | Arg | Tyr | Gln | Glu | Gln | Gly | Gly | Glu | Ala | Ser | Pro | 85  | 90  | 95  |    |
| Gln | Ser | Arg | Thr | Trp | Glu | Gln | Gln | Gln | Glu | Val | Val | Ser | Arg | Asn | Arg | 100 | 105 | 110 |    |
| Asn | Glu | Gln | Glu | Ser | Ala | Val | His | Pro | Arg | Glu | Ile | Phe | Lys | Gln | Lys |     |     |     |    |

| 115                                                                                | 120 | 125 |
|------------------------------------------------------------------------------------|-----|-----|
| Glu Arg Ala Met Ser Thr Thr Ser Ile Ser Ser Pro Gln Pro Gly Lys<br>130 135 140     |     |     |
| Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr Gln Pro Glu Thr His<br>145 150 155 160 |     |     |
| Phe Gly Arg Glu Pro Ala Ala Ala Ile Ser Arg Pro Arg Ala Asp Leu<br>165 170 175     |     |     |
| Pro Ala Glu Glu Pro Ala Pro Ser Thr Pro Pro Cys Leu Val Gln Ala<br>180 185 190     |     |     |
| Glu Glu Glu Ala Val Tyr Glu Glu Pro Pro Glu Gln Glu Thr Phe Tyr<br>195 200 205     |     |     |
| Glu Gln Pro Pro Leu Val Gln Gln Gln Gly Ala Gly Ser Glu His Ile<br>210 215 220     |     |     |
| Asp His His Ile Gln Gly Gln Gly Leu Ser Gly Gln Gly Leu Cys Ala<br>225 230 235 240 |     |     |
| Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr Glu Ile Ser Phe<br>245 250 255     |     |     |
| Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile Asp Glu Gly Trp<br>260 265 270     |     |     |
| Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met Phe Pro Ala Asn<br>275 280 285     |     |     |
| Tyr Val Glu Leu Ile Asp Glu Ala Glu Gly Thr Ser Cys Pro Ser Pro<br>290 295 300     |     |     |
| Leu Arg His Gly Phe Leu Ile Ala Gly Arg Gly Gly Leu Gly Val Asp<br>305 310 315 320 |     |     |
| Ile Gln His Ser Ser Arg Asn Arg Thr Pro Ser Glu Asp Glu Ala Ser<br>325 330 335     |     |     |
| Gly Leu Pro Pro Ala Trp Gln Thr Gln Pro Val Thr Pro Asn Ala Ala<br>340 345 350     |     |     |
| Met Ala Trp<br>355                                                                 |     |     |

(2). INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2873 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCGGCCGCGT CGACATTGAA AGGAAAAGAT TAGAACTAAT GCAGAAAAAG AAAC TAGAAG | 60  |
| ATGAGGCTGC AAGGAAAGCA AAGCAAGGAA AAGAAAAC TTATGGAAAGAA AATCTTAGAA  | 120 |
| AGGAGGAAGA AGAAAAACAA AAGCGACTCC AGGAAGAAAA AACACAAGAA AAAATTCAAG  | 180 |
| AAGAGGAACG GAAAGCTGAG GAGAAACAAC GTGAGACAGC TAGTGT TTTC GTGAATTATA | 240 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| GAGCATTATA | CCCCTTTGAA | GCAAGGAACC | ATGATGAGAT  | GAGTTTTAAT | TCTGGAGATA | 300  |
| TAATTCAGGT | TGATGAAAAA | ACCGTAGGAG | AACCTGGTTG  | GCTTTATGGT | AGTTTTCAAG | 360  |
| GAAATTTTGG | CTGGTTTCCA | TGCAATTATG | TAGAAAAAAT  | GCCATCAAGT | GAAAATGAAA | 420  |
| AAGCTGTATC | TCCAAAGAAG | GCCTTACTTC | CTCCTACAGT  | TTCTTTATCT | GCTACCTCAA | 480  |
| CTTCCTCTGA | ACCACTTTCT | TCAAATCAAC | CAGCATCAGT  | GACTGATTAT | CAAAATGTAT | 540  |
| CTTTTTTCAA | CCTAACTCTA | AATACATCAT | GGCAGAAAAA  | ATCAGCCTTC | ACTCGAACTG | 600  |
| TGTCCCTGG  | ATCTGTATCA | CCTATTCATG | GACAGGGACA  | AGTGGTAGAA | AACTTAAAG  | 660  |
| CACAGGCCCT | TTGTTCTGG  | ACTGCAAAGA | AAGATAACCA  | CTTGAACCTC | TCAAAACATG | 720  |
| ACATTATTAC | TGTCTTGGAG | CAGCAAGAAA | ATTGGTGGTT  | TGGGGAGGTG | CATGGAGGAA | 780  |
| GAGGATGGTT | TCCCAAATCT | TATGTCAAGA | TCATTCCTGG  | GAGTGAAGTA | AAACGGGAAG | 840  |
| AACCAGAAGC | TTTGTATGCA | GCTGTAAATA | AGAAACCTAC  | CTCGGCAGCC | TATTCAGTTG | 900  |
| GAGAAGAATA | TATTGCACTT | TATCCATATT | CAAGTGTGGA  | ACCTGGAGAT | TTGACTTTCA | 960  |
| CAGAAGGTGA | AGAAATATTG | GTGACCCAGA | AAGATGGAGA  | GTGGTGGACA | GGAAGTATTG | 1020 |
| GAGATAGAAG | TGGAATTTTT | CCATCAAAC  | ATGTCAAACC  | AAAGGATCAA | GAGAGTTTTG | 1080 |
| GGAGTGCTAG | CAAGTCTGGA | GCATCAAATA | AAAAACCTGA  | GATTGCTCAG | GTAACCTCAG | 1140 |
| CATATGTTGC | TTCTGGTTCT | GAACAACTTA | GCCTTGCACC  | AGGACAGTTA | ATATTAATTC | 1200 |
| TAAAGAAAAA | TACAAGTGGG | TGGTGGCAAG | GAGAGTTACA  | GGCCAGAGGA | AAAAAGCGAC | 1260 |
| AGAAAGGATG | GTTTCCTGCC | AGTCATGTTA | AACTTTTGGG  | TCCAAGTAGT | GAAAGAGCCA | 1320 |
| CACCTGCCTT | TCATCCTGTA | TGTCAGGTGA | TTGCTATGTA  | TGACTATGCA | GCAAATAATG | 1380 |
| AAGATGAGCT | CAGTTTCTCC | AAGGGACAAC | TCATTAATGT  | TATGAACAAA | GATGATCCTG | 1440 |
| ATTGGTGGCA | AGGAGAGATC | AACGGGGTGA | CTGGTCTCTT  | TCCTTCAAAC | TACGTTAAGA | 1500 |
| TGACGACAGA | CTCAGATCCA | AGTCAACAGT | GACCCAATGT  | TGTCTTCCAG | TTGTGAAAGC | 1560 |
| ACCCAGAGA  | CCCACTATCC | AAGTTTCACT | CTAGCGTGGA  | GGCAGGGCAG | GCAGCCCTGA | 1620 |
| TCAAATATCT | CCTACACAAT | TCGTTTACTT | CGTTTGAATG  | TTAGAGCCAC | TTGTGATTAT | 1680 |
| TTTTTTGTGT | TTCTAACTTA | CAGTTTAAAT | TTATTTGTAA  | AAAGTTAAAG | GATAGTGGGT | 1740 |
| CTTTGTGTGG | CTTTCCTGTC | TGTTCACTCT | GGCATCTTTA  | GCATTTTCT  | TCTTTTTTAA | 1800 |
| TTTGATAATT | GTAGGTCATT | AGCATGCATA | TTGAGTTTGC  | CCTTATGTGG | TGGGAGTTCA | 1860 |
| AACACACAAA | GACCCACTAT | TTGCACAAAC | TATTCTTACT  | GGTTTGGAAT | AGGCTGCCAT | 1920 |
| GCTTTTTTAA | TGTTATTGCA | ACATGTGTAT | TCATTTACAG  | AATTCAGATA | AAATTTGCTT | 1980 |
| ATGTTCTGCT | ATTATGTTTG | ATCTAATCCT | AATCACAGTG  | AGCTCTTAAT | TAGCTCAATA | 2040 |
| TGTGGTTTGC | CCTCAAGTGT | GCACTGTTTA | TTACTTTGTA  | ATATGCCACT | ATGAGTACTG | 2100 |
| ACATTTAGAT | ATGTTTAAAG | GCCAAGAACT | GGAAACAGCC  | ATGCCCTGTT | TTCTGTGTAT | 2160 |
| TTGGGATGGG | AATAACAACA | TTTTGGGGGG | AGCTTTTTTAA | ATCTCAGAGA | AGAGGAAAGT | 2220 |
| GGCCTGCTCT | GGCAGGTATG | TGCAGTGTTT | CATTTGTTCC  | AGTCCAAGA  | ATGAGCACTG | 2280 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| TCCTATGGTA GTTCGCTTAG GATCTTTATG TGCTCTGGGC TAATGAAGGT ACTGCATCAT   | 2340 |
| GTGCTGCAGC GTGTGTATTC TTTTTCGATG ACCTATAAAG GGATTATTTT TGAGGAATGA   | 2400 |
| AAGGCTCCCA TCATTGACTG TGAGATGGGA AAAACCTTTC CTAGCTTAGA GCATTTATAT   | 2460 |
| CTTAATCCAT TTAAAGTCA GAGTTCATTG TTACCTGTTT TAATCAGGTG ACTACATGTC    | 2520 |
| CCAGTATACA AAGGGGCACT GGTGACATT CTTCTTAATG TATTTAGTAA ATATCATAAG    | 2580 |
| AAATCCTTTA AGAGTTTAAA TGTCCCCAAA ACAGACATGC GGGCTCTAGT CAAGAATGAA   | 2640 |
| TTAGAGTGAA GGAAAGCTGT GTAACACCTG GCATTCCCTCT GTGTTTCATGG AGCTTCTTTG | 2700 |
| AGGCTCTAAG ATTGATTTTA CCATCAGACT TCTCTAATAC CTGTTCTTCA ACCATATTGG   | 2760 |
| CTACTTTGAC ATAAGAATTT ACTTCTTTTC CTGGAATGGA AAACACTTTA AAAAATAATA   | 2820 |
| ACAAACATTA TTATAAACTA ATATATGTGA GAGGTCGACG CGGCCGCGAA TTC          | 2873 |

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 509 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Val | Asp | Ile | Glu | Arg | Lys | Arg | Leu | Glu | Leu | Met | Gln | Lys | Lys | 1   | 5   | 10  | 15  |
| Lys | Leu | Glu | Asp | Glu | Ala | Ala | Arg | Lys | Ala | Lys | Gln | Gly | Lys | Glu | Asn | 20  | 25  | 30  |     |
| Leu | Trp | Lys | Glu | Asn | Leu | Arg | Lys | Glu | Glu | Glu | Glu | Lys | Gln | Lys | Arg | 35  | 40  | 45  |     |
| Leu | Gln | Glu | Glu | Lys | Thr | Gln | Glu | Lys | Ile | Gln | Glu | Glu | Glu | Arg | Lys | 50  | 55  | 60  |     |
| Ala | Glu | Glu | Lys | Gln | Arg | Glu | Thr | Ala | Ser | Val | Leu | Val | Asn | Tyr | Arg | 65  | 70  | 75  | 80  |
| Ala | Leu | Tyr | Pro | Phe | Glu | Ala | Arg | Asn | His | Asp | Glu | Met | Ser | Phe | Asn | 85  | 90  | 95  |     |
| Ser | Gly | Asp | Ile | Ile | Gln | Val | Asp | Glu | Lys | Thr | Val | Gly | Glu | Pro | Gly | 100 | 105 | 110 |     |
| Trp | Leu | Tyr | Gly | Ser | Phe | Gln | Gly | Asn | Phe | Gly | Trp | Phe | Pro | Cys | Asn | 115 | 120 | 125 |     |
| Tyr | Val | Glu | Lys | Met | Pro | Ser | Ser | Glu | Asn | Glu | Lys | Ala | Val | Ser | Pro | 130 | 135 | 140 |     |
| Lys | Lys | Ala | Leu | Leu | Pro | Pro | Thr | Val | Ser | Leu | Ser | Ala | Thr | Ser | Thr | 145 | 150 | 155 | 160 |
| Ser | Ser | Glu | Pro | Leu | Ser | Ser | Asn | Gln | Pro | Ala | Ser | Val | Thr | Asp | Tyr | 165 | 170 | 175 |     |
| Gln | Asn | Val | Ser | Phe | Ser | Asn | Leu | Thr | Val | Asn | Thr | Ser | Trp | Gln | Lys |     |     |     |     |

| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Lys | Ser | Ala | Phe | Thr | Arg | Thr | Val | Ser | Pro | Gly | Ser | Val | Ser | Pro | Ile |  |  |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |  |  |
| His | Gly | Gln | Gly | Gln | Val | Val | Glu | Asn | Leu | Lys | Ala | Gln | Ala | Leu | Cys |  |  |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |  |  |
| Ser | Trp | Thr | Ala | Lys | Lys | Asp | Asn | His | Leu | Asn | Phe | Ser | Lys | His | Asp |  |  |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |  |  |
| Ile | Ile | Thr | Val | Leu | Glu | Gln | Gln | Glu | Asn | Trp | Trp | Phe | Gly | Glu | Val |  |  |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |  |  |
| His | Gly | Gly | Arg | Gly | Trp | Phe | Pro | Lys | Ser | Tyr | Val | Lys | Ile | Ile | Pro |  |  |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |  |  |
| Gly | Ser | Glu | Val | Lys | Arg | Glu | Glu | Pro | Glu | Ala | Leu | Tyr | Ala | Ala | Val |  |  |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |  |  |
| Asn | Lys | Lys | Pro | Thr | Ser | Ala | Ala | Tyr | Ser | Val | Gly | Glu | Glu | Tyr | Ile |  |  |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |  |  |
| Ala | Leu | Tyr | Pro | Tyr | Ser | Ser | Val | Glu | Pro | Gly | Asp | Leu | Thr | Phe | Thr |  |  |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |  |  |
| Glu | Gly | Glu | Glu | Ile | Leu | Val | Thr | Gln | Lys | Asp | Gly | Glu | Trp | Trp | Thr |  |  |  |  |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |  |  |
| Gly | Ser | Ile | Gly | Asp | Arg | Ser | Gly | Ile | Phe | Pro | Ser | Asn | Tyr | Val | Lys |  |  |  |  |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |  |  |
| Pro | Lys | Asp | Gln | Glu | Ser | Phe | Gly | Ser | Ala | Ser | Lys | Ser | Gly | Ala | Ser |  |  |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |  |  |
| Asn | Lys | Lys | Pro | Glu | Ile | Ala | Gln | Val | Thr | Ser | Ala | Tyr | Val | Ala | Ser |  |  |  |  |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |  |  |
| Gly | Ser | Glu | Gln | Leu | Ser | Leu | Ala | Pro | Gly | Gln | Leu | Ile | Leu | Ile | Leu |  |  |  |  |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |  |  |
| Lys | Lys | Asn | Thr | Ser | Gly | Trp | Trp | Gln | Gly | Glu | Leu | Gln | Ala | Arg | Gly |  |  |  |  |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |  |  |
| Lys | Lys | Arg | Gln | Lys | Gly | Trp | Phe | Pro | Ala | Ser | His | Val | Lys | Leu | Leu |  |  |  |  |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |  |  |  |
| Gly | Pro | Ser | Ser | Glu | Arg | Ala | Thr | Pro | Ala | Phe | His | Pro | Val | Cys | Gln |  |  |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |  |  |
| Val | Ile | Ala | Met | Tyr | Asp | Tyr | Ala | Ala | Asn | Asn | Glu | Asp | Glu | Leu | Ser |  |  |  |  |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |  |  |
| Phe | Ser | Lys | Gly | Gln | Leu | Ile | Asn | Val | Met | Asn | Lys | Asp | Asp | Pro | Asp |  |  |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |  |  |  |  |
| Trp | Trp | Gln | Gly | Glu | Ile | Asn | Gly | Val | Thr | Gly | Leu | Phe | Pro | Ser | Asn |  |  |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |  |  |
| Tyr | Val | Lys | Met | Thr | Thr | Asp | Ser | Asp | Pro | Ser | Gln | Gln |     |     |     |  |  |  |  |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     |     |     |     |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 543 bases

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAATTCGTCG ACCCACGCGT CCGAAATATA ACTGAAGTTG GGGCACCTAC TGAAGAAGAG | 60  |
| GAAGAAAGTG AAAGTGAAGA TAGTGAAGAC AGTGGTGGGG AGGAAGAAGA TGCAGAGGAG | 120 |
| GAAGAGGAAG AGAAAGAGGA AAATGAATCT CACAAATGGT CAACCGGTGA AGAATACATC | 180 |
| GCTGTTGGAG ATTTTACTGC TCAGCAAGTT GGAGATCTTA CATTTAAGAA AGGGGAAATT | 240 |
| CTCCTTGTA TGTGAAAAA ACCTGATGGT TGGTGGATAG CTAAGGATGC CAAAGGAAAT   | 300 |
| GAAGGTCTTG TTCCAGAAC CTACCTAGAG CCTTATAGTG AAGAAGAAGA AGGCCAAGAG  | 360 |
| TCAAGTGAAG AGGGCAGTGA AGAAGATGTA GAGGCGGTGG ATGAAACAGC AGATGGAGCA | 420 |
| GAAGTTAAGC AAAGAACTGA TCCCCACTGG AGTGCTGTTT AGAAAGCGAT TTCAGAGGCG | 480 |
| GGCATCTTCT GTCTTGTTAA TCATGTCTCG TTTGCTACC TAATAGTTCT GATCCGTCCC  | 540 |
| TAA                                                               | 543 |

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| Glu Phe Val Asp Pro Arg Val Arg Asn Ile Thr Glu Val Gly Ala Pro | 1   | 5   | 10  | 15 |
| Thr Glu Glu Glu Glu Glu Ser Glu Ser Glu Asp Ser Glu Asp Ser Gly | 20  | 25  | 30  |    |
| Gly Glu Glu Glu Asp Ala Glu Glu Glu Glu Glu Lys Glu Glu Asn     | 35  | 40  | 45  |    |
| Glu Ser His Lys Trp Ser Thr Gly Glu Glu Tyr Ile Ala Val Gly Asp | 50  | 55  | 60  |    |
| Trp Thr Ala Gln Gln Val Gly Asp Leu Thr Phe Lys Lys Gly Glu Ile | 65  | 70  | 75  | 80 |
| Leu Leu Val Ile Glu Lys Lys Pro Asp Gly Trp Trp Ile Ala Lys Asp | 85  | 90  | 95  |    |
| Ala Lys Gly Asn Glu Gly Leu Val Pro Arg Thr Tyr Leu Glu Pro Tyr | 100 | 105 | 110 |    |
| Ser Glu Glu Glu Glu Gly Gln Glu Ser Ser Glu Glu Gly Ser Glu Glu | 115 | 120 | 125 |    |
| Asp Val Glu Ala Val Asp Glu Thr Ala Asp Gly Ala Glu Val Lys Gln | 130 | 135 | 140 |    |



Arg Thr Asp Pro His Trp Ser Ala Val Gln Lys Ala Ile Ser Glu Ala  
 145 150 155 160  
 Gly Ile Phe Cys Leu Val Asn His Val Ser Phe Cys Tyr Leu Ile Val  
 165 170 175  
 Leu Ile Arg Pro  
 180

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAATTCGGCG GACTTGCGGG CCGCGTCGAC GAAGAAACCT GAAGGACACA CTAGGCCTCG | 60  |
| GCAAGACGCG CAGGAAGACC AGCGCGCGGG ATGCGTCCCC CACGCCCAGC ACGGACGCCG | 120 |
| AGTACCCCGC CAATGGCAGC GGCGCCGACC GCATCTACGA CCTCAACATC CCGGCCTTCG | 180 |
| TCAAGTTCGC CTATGTGGCC GAGCGGGAGG ATGAGTTGTC CCTGGTGAAG GGGTCGCGCG | 240 |
| TCACCGTCAT GGAGAAGTGC AGCGACGGTT GGTGGCGGGG CAGCTACAAC GGGCAGATCG | 300 |
| GCTGGTTCCC CTCCAACCTAC GTCTTGAGG AGGTGGACGA GGCGGTTGCG GAGTCCCCAA | 360 |
| GCTTCCTGAG CCTGCGCAAG GGCGCCTCGC TGAGCAATGG CCAGGGCTCC CGCGTGCTGC | 420 |
| ATGTGGTCCA GACGCTGTAC CCCTTCAGCT CAGTCACCGA GGAGGAGCTC AAGTTCGAGA | 480 |
| AGGGGGAGAC CATGGAGGTG ATTGAGAAGC CGGAGAACGA CCCCAGGTGG TGGAAATGCA | 540 |
| AAAATGCCCC GGGCCAGGTG GGCCTCGTCC CCAAAAATA CGTGGTGGTC CTCAGTGACG  | 600 |
| GGCCTGCCCT GCACCCTGCG CACGCCCCAC AGATAAGCTA CACCGGGCCC TCGTCGAGCG | 660 |
| GCGCTTCGCG GGGCAGAGAG TGGTACTACG GGAACGTGAC GCGGCACCAG GCCGAGTGCG | 720 |
| CCCTCAACGA GCGGGGCGTG GAGGGCGACT TCCTCATTAG GGACAGCGAG TCCTCGCCCA | 780 |
| GCGACTTCTC CGTGTCCCTT AAAGCGTCAG GGAAGAACAA ACACTTCAAG GTGCAGCTCG | 840 |
| TGGACAATGT CTAATGCATT GGGCAGCGGC GCTTCCACAC CATGGACGAG CTGGTGGAAC | 900 |
| ACTACAAAAA GGCGCCCATC TTCACCAGCG AGCACGGGGA GAAGCTCTAC CTCGTCAGGG | 960 |
| CCCTGCAGTG A                                                      | 971 |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ile Arg Arg Thr Ser Arg Pro Arg Arg Arg Arg Asn Leu Lys Asp Thr  
1 5 10 15  
Leu Gly Leu Gly Lys Thr Arg Arg Lys Thr Ser Ala Arg Asp Ala Ser  
20 25 30  
Pro Thr Pro Ser Thr Asp Ala Glu Tyr Pro Ala Asn Gly Ser Gly Ala  
35 40 45  
Asp Arg Ile Tyr Asp Leu Asn Ile Pro Ala Phe Val Lys Phe Ala Tyr  
50 55 60  
Val Ala Glu Arg Glu Asp Glu Leu Ser Leu Val Lys Gly Ser Arg Val  
65 70 75 80  
Thr Val Met Glu Lys Cys Ser Asp Gly Trp Trp Arg Gly Ser Tyr Asn  
85 90 95  
Gly Gln Ile Gly Trp Phe Pro Ser Asn Tyr Val Leu Glu Glu Val Asp  
100 105 110  
Glu Ala Val Ala Glu Ser Pro Ser Phe Leu Ser Leu Arg Lys Gly Ala  
115 120 125  
Ser Leu Ser Asn Gly Gln Gly Ser Arg Val Leu His Val Val Gln Thr  
130 135 140  
Leu Tyr Pro Phe Ser Ser Val Thr Glu Glu Glu Leu Asn Phe Glu Lys  
145 150 155 160  
Gly Glu Thr Met Glu Val Ile Glu Lys Pro Glu Asn Asp Pro Glu Trp  
165 170 175  
Trp Lys Cys Lys Asn Ala Arg Gly Gln Val Gly Leu Val Pro Lys Asn  
180 185 190  
Tyr Val Val Val Leu Ser Asp Gly Pro Ala Leu His Pro Ala His Ala  
195 200 205  
Pro Gln Ile Ser Tyr Thr Gly Pro Ser Ser Ser Gly Arg Phe Ala Gly  
210 215 220  
Arg Glu Trp Tyr Tyr Gly Asn Val Thr Arg His Gln Ala Glu Cys Ala  
225 230 235 240  
Leu Asn Glu Arg Gly Val Glu Gly Asp Phe Leu Ile Arg Asp Ser Glu  
245 250 255  
Ser Ser Pro Ser Asp Phe Ser Val Ser Leu Lys Ala Ser Gly Lys Asn  
260 265 270  
Lys His Phe Lys Val Gln Leu Val Asp Asn Val Tyr Cys Ile Gly Gln  
275 280 285  
Arg Arg Phe His Thr Met Asp Glu Leu Val Glu His Tyr Lys Lys Ala  
290 295 300  
Pro Ile Phe Thr Ser Glu His Gly Glu Lys Leu Tyr Leu Val Arg Ala  
305 310 315 320  
Leu Gln

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```
GAATTCGCGG ACTTCGCGGC CGCGTCGACA CCAGTGCAGG TTTTGGGAATA TGGAGAAGCT 60
ATTGCTAAGT TTAAC TTAA TGGTGATACA CAAGTAGAAA TGTCCTTCAG AAAGGGTGAG 120
AGGATCACAC TGCTCCGGCA GGTAGATGAG AACTGGTACG AAGGGAGGAT CCCGGGGACA 180
TCCCGACAAG GCATCTTCCC CATCACCTAC GTGGATCTGA TCAAGCGACC ACTGGTGAAA 240
AACCCTGTGG ATTACATGGA CCTGCCTTTC TCCTCCTCCC CAAGTCGCAG TGCCACTGCA 300
AGCCACAGC AACCTCAAGC CCAGCAGCGA AGAGTCACCC CCGACAGGAG TCAAACCTCA 360
CAAGATTTAT TTAGCTATCA AGCATTATAT AGCTATATAC CACAGAATGA TGATGAGTTG 420
GAACTCCGCG ATGGAGATAT CGTTGATGTC ATGGAAAAAT GTGACGATGG ATGGTTTGTT 480
GGTACTTCAA GAAGGACAAA GCAGTTTGGT ACTTTTCCAG GCAACTATGT AAAACCTTTG 540
TATCTATAA 549
```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
Glu Phe Ala Asp Phe Ala Ala Ala Ser Thr Pro Val Gln Val Leu Glu
1 5 10 15
Tyr Gly Glu Ala Ile Ala Lys Phe Asn Phe Asn Gly Asp Thr Gln Val
20 25 30
Glu Met Ser Phe Arg Lys Gly Glu Arg Ile Thr Leu Leu Arg Gln Val
35 40 45
Asp Glu Asn Trp Tyr Glu Gly Arg Ile Pro Gly Thr Ser Arg Gln Gly
50 55 60
Ile Phe Pro Ile Thr Tyr Val Asp Val Ile Lys Arg Pro Leu Val Lys
65 70 75 80
Asn Pro Val Asp Tyr Met Asp Leu Pro Phe Ser Ser Ser Pro Ser Arg
85 90 95
Ser Ala Thr Ala Ser Pro Gln Gln Pro Gln Ala Gln Gln Arg Arg Val
100 105 110
Thr Pro Gln Arg Ser Gln Thr Ser Gln Asp Leu Phe Ser Tyr Gln Ala
115 120 125
```

Leu Tyr Ser Tyr Ile Pro Gln Asn Asp Asp Glu Leu Glu Leu Arg Asp  
 130 135 140  
 Gly Asp Ile Val Asp Val Met Glu Lys Cys Asp Asp Gly Trp Phe Val  
 145 150 155 160  
 Gly Thr Ser Arg Arg Thr Lys Gln Phe Gly Thr Phe Pro Gly Asn Tyr  
 165 170 175  
 Val Lys Pro Leu Tyr Leu  
 180

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ser Phe Ala Ala Pro Ala Arg Pro Pro Val Pro Pro Arg Lys Ser Arg  
 1 5 10 15  
 Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other

- (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Phe Ser Phe Pro Pro Leu Pro Pro Ala Pro Gly Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ala Pro Pro Val Pro Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro  
1 5 10 15  
Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met  
20 25 30  
Asp Thr Asn Trp Trp Lys Gly Thr Ser Gly Arg Thr Gly Leu Ile Pro  
35 40 45  
Ser Asn Tyr Val Ala Glu Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Thr Gly Glu Glu Tyr Ile Ala Val Gly Asp Phe Thr Ala Gln Gln Val  
1 5 10 15  
Gly Asp Leu Thr Phe Lys Lys Gly Glu Ile Leu Leu Val Ile Glu Lys  
20 25 30  
Lys Pro Asp Gly Trp Trp Ile Ala Lys Asp Ala Lys Gly Asn Glu Gly  
35 40 45  
Leu Val Pro Arg Thr Tyr Leu Glu Pro Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Glu  
 1 5 10 15  
 Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys  
 20 25 30  
 Asn Asp Asp Gly Trp Tyr Glu Gly Val Met Asn Gly Thr Val Gly Leu  
 35 40 45  
 Ser Pro Gly Asn Tyr Val Glu Ser Ile  
 50 55

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Leu Asn Ile Pro Ala Phe Val Lys Phe Ala Tyr Val Ala Glu Arg Glu  
 1 5 10 15  
 Asp Glu Leu Ser Leu Val Lys Gly Ser Arg Val Thr Val Met Glu Lys  
 20 25 30  
 Cys Ser Asp Gly Trp Trp Arg Gly Ser Tyr Asn Gly Gln Ile Gly Trp  
 35 40 45  
 Phe Pro Ser Asn Tyr Val Leu Glu Glu  
 50 55

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Val Leu His Val Val Gln Thr Leu Tyr Pro Phe Ser Ser Val Thr Glu  
 1 5 10 15  
 Glu Glu Leu Asn Glu Phe Glu Lys Gly Glu Thr Met Glu Val Ile Glu  
 20 25 30  
 Lys Pro Glu Asn Asp Pro Glu Trp Trp Lys Cys Lys Asn Ala Arg Gly  
 35 40 45  
 Gln Val Gly Leu Val Pro Lys Asn Tyr Val Val Val Leu  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

Glu Glu Val Val Val Val Ala Lys Phe Asp Tyr Val Ala Gln Gln Glu
1 5 10 15
Gln Glu Leu Asp Ile Lys Lys Asn Glu Arg Leu Trp Leu Leu Asp Asp
20 25 30
Ser Lys Ser Trp Trp Arg Val Arg Asn Ser Met Asn Lys Thr Gly Phe
35 40 45
Val Pro Ser Asn Tyr Val Glu Arg Lys
50 55

```

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

Leu Met Asn Pro Ala Tyr Val Lys Phe Asn Tyr Met Ala Glu Arg Glu
1 5 10 15
Asp Glu Leu Ser Leu Ile Lys Gly Thr Lys Val Ile Val Met Glu Lys
20 25 30
Ile Cys Ser Asp Gly Trp Trp Thr Gly Ser Tyr Asn Gly Gln Val Gly
35 40 45
Trp Phe Pro Ser Asn Tyr Val Thr Glu Glu
50 55

```

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

Val Leu His Val Val Gln Ala Leu Tyr Pro Phe Ser Ser Ser Asn Asp
1 5 10 15
Glu Glu Leu Asn Phe Glu Lys Gly Asp Val Met Asp Val Ile Glu Lys
20 25 30
Pro Glu Asn Asp Pro Glu Trp Trp Lys Cys Arg Lys Ile Asn Gly Met
35 40 45

```

Val Gly Leu Val Pro Lys Asn Tyr Val Thr Val Met  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Asp Leu Phe Ser Tyr Gln Ala Leu Tyr Ser Tyr Ile Pro Gln Asn Asp  
 1 5 10 15  
 Asp Glu Leu Glu Leu Arg Asp Gly Asp Ile Val Asp Val Met Glu Lys  
 20 25 30  
 Cys Asp Asp Gly Trp Phe Val Gly Thr Ser Arg Arg Thr Lys Gln Phe  
 35 40 45  
 Gly Thr Phe Pro Gly Asn Tyr Val Lys Pro Leu  
 50 55

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Gln Gly Arg Lys Glu Arg Ala Arg Tyr Asp Leu Glu Ala Ala Gln Asp  
 1 5 10 15  
 Asn Glu Leu Thr Phe Lys Ala Gly Glu Ile Met Thr Val Leu Asp Asp  
 20 25 30  
 Ser Asp Pro Asn Trp Trp Lys Gly Glu Arg His Gln Gly Ile Gly Leu  
 35 40 45  
 Phe Pro Ser Asn Phe Val Thr Ala Asp  
 50 55

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp



1                      5                      10                      15  
 Thr Glu Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val  
                     20                      25                      30  
 Ile Asp Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly  
                     35                      40                      45  
 Met Phe Pro Ala Asn Tyr Val Glu Leu Ile  
                     50                      55

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Leu Val Leu Asn Tyr Thr Ala Leu Tyr Pro Phe Glu Ala Arg Asn His  
 1                      5                      10                      15  
 Cys Glu Met Ser Phe Asn Ser Gly Asp Ile Ile Gln Val Asp Glu Lys  
                     20                      25                      30  
 Thr Val Gly Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Asn Phe  
                     35                      40                      45  
 Gly Trp Phe Pro Cys Asn Tyr Val Glu Lys Met  
                     50                      55

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala Lys Lys  
 1                      5                      10                      15  
 Asp Asn His Leu Asn Phe Ser Lys His Asp Ile Ile Thr Val Leu Glu  
                     20                      25                      30  
 Gln Gln Glu Asn Phe Trp Trp Phe Gly Glu Val His Gly Gly Arg Gly  
                     35                      40                      45  
 Trp Phe Pro Lys Ser Tyr Val Lys Ile Ile  
                     50                      55

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr Ser Ser Val Glu Pro  
1 5 10 15  
Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys  
20 25 30  
Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp Arg Ser Gly Ile Phe  
35 40 45  
Pro Ser Asn Tyr Val Lys Pro Lys  
50 55

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser  
1 5 10 15  
Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys  
20 25 30  
Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys  
35 40 45  
Arg Gln Lys Gly Trp Phe Pro Ala Ser Trp Val Lys Leu Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Pro Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Ala Ala Asn Asn Glu  
1 5 10 15  
Asp Glu Leu Ser Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys  
20 25 30  
Asp Asp Pro Asp Trp Trp Gln Gly Glu Ile Asn Gly Val Thr Gly Leu  
35 40 45  
Phe Pro Ser Asn Tyr Val Lys Met Thr

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

AATTCAAGCG CGGGGTCTTT AGGATTTGCA GCTCCAGGAA GCGAGATGTC GAAAGCCGCC 60
ACCCAAACCA GTCAAACCAG GGCAAGTTAA AGTCTTCAGA GCCCTGTATA CGTTTGAACC 120
CAGAACTCCA GATGAATTAT ACTTTGAGGA AGGTGATATT ATCTACATTA CTGACATGAG 180
CGATACCAAT TGGTGGAAAG GCACCTCCAA AGGCAGGACT GGACTAATTC CAAGCAACTA 240
TGTGGCTGAG CAGGCAGAAT CCATTGACAA TCCATTGCAT GAAGCAGCAA AAAGAGGCAA 300
CTTGAGCTGG TTGAGAGAGT GTTTGGACAA CAGAGTGGGT GTTAATGGCT TAGACAAACC 360
TGGAAGCACT GCCTTATACT GGGCTTGCCA CGGGGGCCAC AAAGATATAG TGGAAATGCT 420
ATTTACTCTA CCAAATATTG AACTGAACCA GCAGAACAAG TTGGGAGATA CAGCTTTGCA 480
TGCTGCTGCC TGGAAGGGTT ATGCAGATAT CGTCCAGTTG CTTCTGGCAA AAGGTGCTAG 540
AACAGACTTA AGAAACATTG AGAAGAAGCT GGCCTTCGAC ATGGCTACCA ATGCTGCCTG 600
TGCATCTCTC CTGAAAAAGA AACAGGGAAC AGATGCAGTT CGAACATTAA GCAATGCCGA 660
GGACTATCTC GATGATGAAG ACTCAGATTA A 691

```

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

Asn Ser Ser Ala Gly Ser Leu Gly Phe Ala Ala Pro Gly Ser Glu Met
1 5 10 15
Ser Lys Pro Pro Pro Lys Pro Val Lys Pro Gly Gln Val Lys Val Phe
20 25 30
Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro Asp Glu Leu Tyr Phe
35 40 45
Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met Ser Asp Thr Asn Trp
50 55 60
Trp Lys Gly Thr Ser Lys Gly Arg Thr Gly Leu Ile Pro Ser Asn Tyr
65 70 75 80

```



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Ser Arg Pro Pro Arg Trp Ser Pro Pro Val Pro Leu Pro Thr Ser  
1 5 10 15  
Leu Asp Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 bass pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| TNNNCACTCA | CGTCGGTGGT | GTTGGTACGG | ATCGATTCAA | GCACGAGACG  | AAGACGGAAC | 60  |
| CGGAGCCGGG | CGCGCGGACG | GCGGACGCGG | GTCCTGAGAA | AGCCGAAGAT  | GGCAGTGAAT | 120 |
| GTGTACTCTA | CGTCAGTCAC | CAGTGATAAC | CTAAGTCGAC | ATGACATGCT  | GGCTTGGATC | 180 |
| AATGAATCTC | TGCAGTTGAA | TCTGACAAAG | ATAGAACAGT | TGTGTTTCAGG | GGCTGCATAT | 240 |
| TGTCAGTTTA | TGGACATGCT | CTTCCCTGGA | TCCATTGCCT | TGAAGAAAGT  | GAAATTCCAA | 300 |
| GCTAAGCTAG | AACATGAATA | TATCCAGAAC | TTCAAATAAC | TACAAGCAGG  | CTTCAAGAGG | 360 |
| ATGGGCGTTG | ACAAAATAAT | TCCTGTGGAT | AAATTAGTAA | AAGGAAAATT  | TCAGGACAAT | 420 |
| TTTGAATTTG | TTCAATGGTT | CAAGAAGTTT | TTTGATGCAA | ATTATGATGG  | AAAAGAGTAT | 480 |
| GATCCTGTAG | CTGCCAGACA | AGGTCAAGAA | ACTGCAGTGG | NTCCTTCTCT  | TGTCGCCCCA | 540 |
| GCTTTGAGTA | AACCGAAGAA | ACCTCTCGGN | TCCAGTACTG | CAGNCCCACA  | GAGACCCATT | 600 |
| GNAACACAGA | GGACTACTGC | AGNTCCTAAG | GNTGGCCCCG | GAATGGTGCG  | AAAGAATCCT | 660 |
| GGTGTGGNNA | ATGGAGGATG | ATGANGCAGC | TNT        |             |            | 693 |

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Arg Ile Asp Ser Ser Thr Arg Arg Arg Arg Asn Arg Ser Arg Ala Arg  
1 5 10 15  
Gly Arg Arg Thr Arg Val Leu Arg Lys Pro Lys Met Ala Val Asn Val  
20 25 30  
Tyr Ser Thr Ser Val Thr Ser Asp Asn Leu Ser Arg His Asp Met Leu  
35 40 45  
Ala Trp Ile Asn Glu Ser Leu Asn Leu Gln Leu Thr Lys Ile Glu Gln  
50 55 60  
Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro  
65 70 75 80  
Gly Ser Ile Ala Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His  
85 90 95  
Glu Tyr Ile Gln Asn Phe Lys Ile Leu Gln Ala Gly Phe Lys Arg Met  
100 105 110  
Gly Val Asp Lys Ile Ile Pro Val Asp Lys Leu Val Lys Gly Lys Phe  
115 120 125  
Gln Asp Asn Phe Glu Phe Val Gln Trp Phe Lys Lys Phe Phe Asp Ala  
130 135 140  
Asn Tyr Asp Gly Lys Glu Tyr Asp Pro Val Ala Ala Arg Gln Gly Gln  
145 150 155 160  
Glu Thr Ala Val Xaa Pro Ser Leu Val Ala Pro Ala Leu Ser Lys Pro  
165 170 175  
Lys Lys Pro Leu Gly Ser Ser Thr Ala Xaa Pro Gln Arg Pro Ile Xaa  
180 185 190  
Thr Gln Arg Thr Thr Ala Xaa Pro Lys Xaa Gly Pro Gly Met Val Arg  
195 200 205  
Lys Asn Pro Gly Val Xaa Asn Gly Gly  
210 215

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Ser Gly Ser Gly Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu  
1 5 10 15  
Val

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly Asp Gly Tyr Leu Glu Leu Ser Pro  
1 5